ECOSYSTEM SURVEILLANCE (AusPlots) TUTORIAL: UNDERSTANDING AND USING THE 'ausplotsR' PACKAGE AND AusPlots DATA

This document contains a tutorial on how to access and use TERN's Ecosystem Surveillance (AusPlots) data.We will explore the use of both the package 'ausplotsR' & the 'ausplots' data that can be downloaded with this package.

`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 cover, growth form, and basal area.

In this section of the workshop we will cover the following aspects:

1. ACCESSING AND INSTALLING THE `ausplotsR` PACKAGE (plus its Dependencies).
2. OBTAIN & EXPLORE AusPlots DATA: `get_ausplots` function:

- `get_ausplots` function
- Explore the structure of the obtained AusPlots data.

3. MANIPULATING AusPlots DATA:

- Find the 5 most sampled Bioregions.
- Subset sites in the 5 most sampled Bioregions (in all DFs in the list)

4. MAP THE SITES

- Obtain and prepare a map of Australia
- Plot AusPlots sites in the 5 most sampled Bioregions on the map of Australia.

5. SPECIES-LEVEL DATA: `species_table` function and species occurrence matrices (for the 5 most sampled Bioregions).

- First step: Create a species occurrence matrix. Compute Species by Site table using the function `species_table`
- Species Abundance/Percent Cover:
    - Percent Cover (Abundance) by Site Visit x Species (i.e. in all 'cells')
    - Abundance (Cover %) by Species. Find and plot 4 most abundant species on a map (dot size proportional to Abundance).
- Species Occurrence (Presence/Absence):
    - Presence/Absence across all Cells (i.e. Site Visit x Species).
    - Total Presence/Absence for each Species (i.e. per data frame Column):
        - Frequencies: Absolute and Relative.
        - Calculate and Plot (histogram): Presence (Absolute and Relative) Frequencies.
- Species Diversity:
    - Calculate various indices and create a data frame with these indices.
    - Plot 2 indices: Species Richness (from vouchers, more species recorded), and Shannon Index (from veg.PI for abundances) on a map (dot size proportional to the relevant diversity metric) .
- Rank-Abundance Curves (= Whittaker Plots) & Relative Abundance Models
    - Rank-Abundance Curves for the First 5 Site-Visits
    - Possible Models of Relative Abundance for one Community
    - Rank-Abundance Curves for each Bioregion (using the Species Mean Cover)

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

- Latitudinal pattern in proportional vegetation cover (for a random subset of 200 sites).
- Temporal Variation in Fractional Cover: Explore, display, and assess (for 5 sites visited twice).

7. GROWTH FORM: `growth_form_table` function (for 5 most sampled bioregions)

- Plant Growth Forms Percent Cover against Sites : Compute using `growth_form_table`
- Cluster (Hierarchical Clustering) by Plant Growth Forms Percent Cover, colour branches by bioregion.

8. TOTAL VEGETATION COVER BY GROWTH FORM AND/OR HEIGHT: `single_cover_value` function (for 5 most sampled bioregions).

- Total Vegetation Cover of Any Green Vegetation >= 2m in Height
- Total Vegetation Cover of Trees >= 5m in Height (i.e. default arguments)
- Total Vegetation Cover of "Tussoc grass" of any Height (i.e. >= 0m height)

9. BASAL AREA (OR NUMBER OF BASAL WEDGE HITS): `basal_area` function (for 5 most sampled bioregions).

- Basal Area for each plot (m2/ha): Compute using `basal_area` .
- Display Basal Areas on map of Australia (dots size proportional to Basal Area).
- Boxplot of Basal Areas by Bioregion.

REQUIRED LIBRARIES

To run the R scripts in this tutorial a number of R packages (and their dependencies) must be installed. In addition to `ausplotsR` , which is at the core of this tutorial, the following packages are required: `dendextend` , `ggplot2` , `goeveg` , `gridExtra` , `mapdata` , `maps` , `maptools` , `sp` , and `vegan` .

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 function `install.packages` (selecting the CRAN mirror using the argument `repos`). Typically 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 (https://cran.r-project.org/mirrors.html).

This is how you can install and load the R packages required for this tutorial.

If you need to install any of the required packages but `ausplotsR`, which is a special case (see below), uncomment the script below.

```
## 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

## Install other required libraries
#install.packages(c("ausplotsR", "vegan", "goeveg", "maps", "maptools", "mapdata", "sp", ggpl
ot2", "gridExtra", "ggspatial", "dendextend"), repos=my.repos)
```

Now the packages can be loaded using the `library` command.

```
# Load packages
library(ausplotsR)  # If not loaded above
library(vegan)
library(goeveg)

library(maps)
library(maptools)
library(mapdata)
library(sp)
library(ggplot2)
library(gridExtra)
#library(ggspatial)

library(dendextend)
```

ACCESSING AND INSTALLING THE `ausplotsR` PACKAGE (plus its Dependencies)

Currently `ausplotsR` must be installed directly from github using the 'devtools' package, which must have been previously installed. The GitHub site for `ausplotsR` contains the latest developments and information on the package; it can be found in this link (https://github.com/ternaustralia/ausplotsR).

```
## 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\RtmpyGuJRi\downloaded_packages
```

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

## Load the package
library(ausplotsR)

## Obtaining Help and Initial Steps
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.
- `structural_summaries` : Site vegetation structural summaries
- `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.
- `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.
- `basal.wedge` : Basal Wedge Data Raw Hits. These data are required for the calculation of Basal Area by Species by Plot.
- `soil_subsites` : Information on what soil and soil metagenomics samples were taken at nine locations across the plot and their identification barcode numbers.
- `soil_bulk_density` :
- `soil_character` : Soil characterisation and sample ID data at 10 cm increments to a depth of 1 m.

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). If `veg.vouch=TRUE` , which is the default, `veg.vouch` will return a data frame that only includes voucher records that match the species_name_search.

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 interrelate the 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). We will see multiple examples of data frame contents merges later in this tutorial. The variable 'site_unique' is typically the best option to link data frames, 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':   3 obs. of  43 variables:
##   ..$ site_location_name        : chr [1:3] "QDAMGD0022" "SATFLB0004" "NTASTU0002"
##   ..$ established_date          : chr [1:3] "2013-06-04T00:00:00" "2012-09-18T00:00:00" "2
016-05-01T16:58:00"
##   ..$ description               : chr [1:3] "Mackunda Downs Station, 500m east of homestea
d.  26km west of Middleton." "Brachina lower" "Maryfield Station, 7.6km north north west of h
omestead. 27.5km south east of Larrimah"
##   ..$ bioregion_name            : chr [1:3] "MGD" "FLB" "STU"
##   ..$ landform_pattern          : chr [1:3] "ALP" "MOU" "PLA"
##   ..$ landform_element          : chr [1:3] "PLA" "HSL" "PLA"
##   ..$ site_slope                : chr [1:3] "1" "35" "0"
##   ..$ site_aspect               : chr [1:3] "180" "225" NA
##   ..$ comments                  : chr [1:3] "Astrebla pectinata / Cenchrus ciliaris / Astr
ebla elymoides low open tussock grassland on alluvial plain adjoin"| __truncated__ "Largely u
nchanged since previous visit possibly more Carrichtera annua. Grazing impact goat, rabbits a
nd kangar"| __truncated__ "Plot is flat. Low mound ( Likely anthropogenic) made up of ironsto
ne gravels at the north west corner. Minimal "| __truncated__
##   ..$ outcrop_lithology         : chr [1:3] "NA" "SA" "NA"
##   ..$ other_outcrop_lithology   : chr [1:3] "NA" NA "NC"
##   ..$ plot_dimensions           : chr [1:3] "100m x 100m." NA NA
##   ..$ site_location_visit_id    : int [1:3] 53501 53705 58429
##   ..$ visit_start_date          : chr [1:3] "2013-05-18T09:34:00" "2012-09-18T00:00:00" "2
016-05-01T16:58:00"
##   ..$ visit_end_date            : chr [1:3] "2013-05-18T09:34:00" "2012-09-18T00:00:00" "2
016-05-01T16:58:00"
##   ..$ visit_notes               : chr [1:3] "" NA "Corymbia polycarpa and Corymbia termina
lis combined for Basal area\r\n\r\nunknown substrate in point intercept "| __truncated__
##   ..$ location_description      : chr [1:3] "Mackunda Station, north of Middleton." "Brach
ina Gorge Heysen Range Lower. 63km North North East of Adelaide" "Maryfield Station, 7.6km no
rth north west of homestead. 27.5km south east of Larimah"
##   ..$ erosion_type              : chr [1:3] "G" "NC" "n/a"
##   ..$ erosion_abundance         : chr [1:3] "2" "NC" "X"
##   ..$ erosion_state             : chr [1:3] "NC" "NC" "n/a"
##   ..$ microrelief               : chr [1:3] "Z" "NC" "TM"
##   ..$ drainage_type             : int [1:3] 4 7 4
##   ..$ disturbance               : chr [1:3] "1L" "NC" "0"
##   ..$ climatic_condition        : chr [1:3] "DRY" "WET" "DRY"
##   ..$ vegetation_condition      : chr [1:3] "DRY" "AVG" "AVG"
##   ..$ observer_veg              : int [1:3] 3 16 1
##   ..$ observer_soil             : int [1:3] 2 1 2
##   ..$ described_by              : int [1:3] 3 16 1
##   ..$ pit_marker_easting        : int [1:3] 529568 839490 326265
##   ..$ pit_marker_northing       : int [1:3] 7526350 6528576 8256078
##   ..$ pit_marker_mga_zones      : int [1:3] 54 53 53
##   ..$ pit_marker_datum          : chr [1:3] "WGS84" "GDA94" "WGS84"
##   ..$ pit_marker_location_method: chr [1:3] "GPS" "GPS" NA
##   ..$ soil_observation_type     : chr [1:3] "P" "P" "P"
##   ..$ a_s_c                     : chr [1:3] "NC" NA NA
##   ..$ plot_is_100m_by_100m      : logi [1:3] TRUE TRUE TRUE
##   ..$ plot_is_aligned_to_grid   : logi [1:3] TRUE TRUE TRUE
##   ..$ plot_is_permanently_marked: logi [1:3] TRUE TRUE TRUE
##   ..$ latitude                  : num [1:3] -22.4 -31.3 -15.8
##   ..$ longitude                 : num [1:3] 141 139 133
##   ..$ point                     : chr [1:3] "SW" "SW" "SW"
##   ..$ state                     : chr [1:3] "QLD" "SA" "NT"
##   ..$ site_unique               : chr [1:3] "QDAMGD0022-53501" "SATFLB0004-53705" "NTASTU0
```

```
002-58429"
##  $ struct.summ  :'data.frame':   3 obs. of  15 variables:
##   ..$ site_location_name    : chr [1:3] "QDAMGD0022" "SATFLB0004" "NTASTU0002"
##   ..$ site_location_visit_id: int [1:3] 53501 53705 58429
##   ..$ phenology_comment     : chr [1:3] "" "Ptilotus obovatus var. obovatus  flowering. Tr
iodia sp. has no seeds. No fruit on Callitris glaucophylla - no e"| __truncated__ "NC"
##   ..$ upper_1_dominant      : chr [1:3] "" "SAT 000251" "NTA017194"
##   ..$ upper_2_dominant      : chr [1:3] "" "SAT 000229" "NTA017232"
##   ..$ upper_3_dominant      : chr [1:3] "" NA "NTA017084"
##   ..$ mid_1_dominant        : chr [1:3] "" "SAT 000244" NA
##   ..$ mid_2_dominant        : chr [1:3] "" "SAT 000261" NA
##   ..$ mid_3_dominant        : chr [1:3] "" NA NA
##   ..$ ground_1_dominant     : chr [1:3] "QDA  003325" "SAT 000233" "NTA017070"
##   ..$ ground_2_dominant     : chr [1:3] "QDA  003293" NA "NTA017076"
##   ..$ ground_3_dominant     : chr [1:3] "QDA  003325" NA "NTA017082"
##   ..$ description           : chr [1:3] "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__
##   ..$ mass_flowering_event  : logi [1:3] FALSE FALSE FALSE
##   ..$ site_unique           : chr [1:3] "QDAMGD0022-53501" "SATFLB0004-53705" "NTASTU0002-
58429"
##  $ soil.subsites:'data.frame':   27 obs. of  12 variables:
##   ..$ site_location_name      : chr [1:27] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAMGD0
022" ...
##   ..$ site_location_visit_id  : int [1:27] 53501 53501 53501 53501 53501 53501 53501 53501
53501 53705 ...
##   ..$ subsite_id              : chr [1:27] "1" "2" "3" "4" ...
##   ..$ zone                    : int [1:27] 54 54 54 54 54 54 54 54 54 53 ...
##   ..$ easting                 : int [1:27] 529581 529580 529582 529592 529595 529620 52966
4 529587 529663 268530 ...
##   ..$ northing                : int [1:27] 7526343 7526338 7526335 7526338 7526345 7526378
7526417 7526423 7526333 6531529 ...
##   ..$ ten_to_twenty_barcode   : chr [1:27] "QDA   051589" "QDA   051592" "QDA   051595" "Q
DA   051598" ...
##   ..$ zero_to_ten_barcode     : chr [1:27] "QDA   051588" "QDA   051591" "QDA   051594" "Q
DA   051597" ...
##   ..$ twenty_to_thirty_barcode: chr [1:27] "QDA   051590" "QDA   051593" "QDA   051596" "Q
DA   051599" ...
##   ..$ comments                : chr [1:27] "bare ground" "between grass tussocks" "between
grass tussocks" "bare ground" ...
##   ..$ metagenomic_barcode     : chr [1:27] "QDA 053721" "QDA 053722" "QDA 053723" "QDA 053
724" ...
##   ..$ site_unique             : chr [1:27] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMGD00
22-53501" "QDAMGD0022-53501" ...
##  $ soil.bulk    :'data.frame':   6 obs. of  15 variables:
##   ..$ site_location_name      : chr [1:6] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "NTASTU00
02" ...
##   ..$ site_location_visit_id  : int [1:6] 53501 53501 53501 58429 58429 58429
##   ..$ sample_id               : chr [1:6] "0" "1" "2" "0" ...
##   ..$ paper_bag_weight        : logi [1:6] NA NA NA NA NA NA
##   ..$ oven_dried_weight_in_bag: logi [1:6] NA NA NA NA NA NA
##   ..$ ring_weight             : logi [1:6] NA NA NA NA NA NA
##   ..$ gravel_weight           : int [1:6] NA NA NA 0 0 0
##   ..$ ring_volume             : num [1:6] NA NA NA 209 209 ...
##   ..$ gravel_volume           : int [1:6] NA NA NA 0 0 0
##   ..$ fine_earth_weight_in_bag: int [1:6] NA NA NA 0 0 0
```

```
##   ..$ fine_earth_weight       : int [1:6] NA NA NA 0 0 0
##   ..$ fine_earth_volume       : num [1:6] NA NA NA 209 209 ...
##   ..$ fine_earth_bulk_density : int [1:6] NA NA NA 0 0 0
##   ..$ gravel_bulk_density     : int [1:6] NA NA NA 0 0 0
##   ..$ site_unique             : chr [1:6] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMGD002
2-53501" "NTASTU0002-58429" ...
##  $ soil.char    :'data.frame':   21 obs. of  34 variables:
##   ..$ site_location_name    : chr [1:21] "SATFLB0004" "QDAMGD0022" "QDAMGD0022" "QDAMGD002
2" ...
##   ..$ site_location_visit_id: int [1:21] 53705 53501 53501 53501 53501 53705 53501 53705 5
3501 53501 ...
##   ..$ upper_depth           : num [1:21] 0 0.5 0.8 0.6 0.7 0.1 0.3 0.6 0.2 0 ...
##   ..$ lower_depth           : num [1:21] 0.1 0.6 0.9 0.7 0.8 0.2 0.4 0.7 0.3 0.1 ...
##   ..$ horizon               : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ texture_grade         : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ texture_qualifier     : chr [1:21] NA "NC" "NC" "NC" ...
##   ..$ texture_modifier      : chr [1:21] NA "NC" "NC" "NC" ...
##   ..$ colour_when_moist     : chr [1:21] NA "NC" "NC" "NC" ...
##   ..$ colour_when_dry       : chr [1:21] NA "NC" "NC" "NC" ...
##   ..$ mottles_colour        : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ mottles_abundance     : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ mottles_size          : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ segregations_abundance: chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ segregations_size     : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ segregations_nature   : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ segregations_form     : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ comments              : chr [1:21] NA NA NA NA ...
##   ..$ collected_by          : int [1:21] 8 4 4 4 4 NA 4 NA 4 4 ...
##   ..$ smallest_size_1       : chr [1:21] "11" "11" "11" "11" ...
##   ..$ smallest_size_2       : logi [1:21] NA NA NA NA NA NA ...
##   ..$ effervescence         : chr [1:21] "N" "N" "N" "N" ...
##   ..$ ec                    : num [1:21] 0.07 0.18 0.54 0.38 0.52 0.03 0.07 1.84 0.06 0.04
...
##   ..$ ph                    : num [1:21] 6.3 8.3 8.1 8.3 8.1 7 8 8.3 7.9 7.8 ...
##   ..$ pedality_grade        : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ pedality_fabric       : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ next_size_type_2      : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ next_size_type_1      : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ smallest_size_type_2  : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ smallest_size_type_1  : chr [1:21] "NC" "NC" "NC" "NC" ...
##   ..$ next_size_2           : logi [1:21] NA NA NA NA NA NA ...
##   ..$ next_size_1           : chr [1:21] "11" "11" "11" "11" ...
##   ..$ layer_barcode         : chr [1:21] "SAT005230" "QDA   051583" "QDA   051586" "QDA
051584" ...
##   ..$ site_unique           : chr [1:21] "SATFLB0004-53705" "QDAMGD0022-53501" "QDAMGD0022
-53501" "QDAMGD0022-53501" ...
##  $ veg.basal    :'data.frame':   70 obs. of  10 variables:
##   ..$ site_location_name     : chr [1:70] "NTASTU0002" "SATFLB0004" "SATFLB0004" "SATFLB00
04" ...
##   ..$ site_location_visit_id : int [1:70] 58429 53705 53705 53705 53705 53705 53705 53705
53705 53705 ...
##   ..$ site_location_id       : int [1:70] 61138 60122 60122 60122 60122 60122 60122 60122
60122 60122 ...
##   ..$ point_id               : chr [1:70] "NE" "W" "SW" "SE" ...
##   ..$ herbarium_determination: chr [1:70] "Dead Tree/Shrub" "Alectryon oleifolius" "Alectr
yon oleifolius" "Alectryon oleifolius" ...
##   ..$ veg_barcode            : chr [1:70] "NO_BARCODE_DEAD_TREE_804159" "SAT 000242" "SAT
000242" "SAT 000242" ...
```

```
##   ..$ hits                  : int [1:70] 1 1 3 4 1 1 1 20 17 6 ...
##   ..$ basal_area_factor     : num [1:70] 0.1 0.25 0.5 0.5 0.5 0.25 0.5 0.25 0.5 0.5 ...
##   ..$ basal_area            : num [1:70] 0.1 0.25 1.5 2 0.5 0.25 0.5 5 8.5 3 ...
##   ..$ site_unique           : chr [1:70] "NTASTU0002-58429" "SATFLB0004-53705" "SATFLB000
4-53705" "SATFLB0004-53705" ...
##  $ veg.vouch    :'data.frame':   149 obs. of  12 variables:
##   ..$ site_location_name       : chr [1:149] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAM
GD0022" ...
##   ..$ veg_barcode              : chr [1:149] "QDA  003331" "NO_BARCODE_FORB_950413164" "N
O_BARCODE_GRASS_656236361" "NO_BARCODE_DEAD_TREE_558409020" ...
##   ..$ herbarium_determination   : chr [1:149] "Glinus lotoides" "Annual forb" "Annual gras
s" "Dead tree/shrub" ...
##   ..$ is_uncertain_determination: logi [1:149] FALSE NA NA NA NA NA ...
##   ..$ visit_start_date          : chr [1:149] "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 [1:149] 53501 53501 53501 53501 53705 53705 53705 53
705 58429 58429 ...
##   ..$ primary_gen_barcode       : chr [1:149] "QDA  003332" NA NA NA ...
##   ..$ secondary_gen_barcode_1   : chr [1:149] NA NA NA NA ...
##   ..$ secondary_gen_barcode_2   : chr [1:149] NA NA NA NA ...
##   ..$ secondary_gen_barcode_3   : chr [1:149] NA NA NA NA ...
##   ..$ secondary_gen_barcode_4   : chr [1:149] NA NA NA NA ...
##   ..$ site_unique               : chr [1:149] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMG
D0022-53501" "QDAMGD0022-53501" ...
##  $ veg.PI       :'data.frame':   3217 obs. of  13 variables:
##   ..$ site_location_name     : chr [1:3217] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAMGD
0022" ...
##   ..$ site_location_visit_id : int [1:3217] 53501 53501 53501 53501 53501 53501 53501 5350
1 53501 53501 ...
##   ..$ transect               : Factor w/ 15 levels "E2-W2","E4-W4",..: 1 13 13 13 13 13 13
13 13 13 ...
##   ..$ point_number           : int [1:3217] 13 3 4 5 6 7 8 9 10 11 ...
##   ..$ veg_barcode            : chr [1:3217] NA "QDA  003325" NA "QDA  003325" ...
##   ..$ herbarium_determination: chr [1:3217] NA "Astrebla pectinata" NA "Astrebla pectinat
a" ...
##   ..$ substrate              : chr [1:3217] "Bare" "Litter" "Bare" "Bare" ...
##   ..$ in_canopy_sky          : logi [1:3217] NA FALSE NA FALSE NA NA ...
##   ..$ dead                   : logi [1:3217] NA FALSE NA FALSE NA NA ...
##   ..$ growth_form            : chr [1:3217] NA "Tussock grass" NA "Tussock grass" ...
##   ..$ height                 : num [1:3217] NA 0.2 NA 0.2 NA NA NA 0.1 NA NA ...
##   ..$ hits_unique            : chr [1:3217] "E2-W2 13" "W1-E1 3" "W1-E1 4" "W1-E1 5" ...
##   ..$ site_unique            : chr [1:3217] "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) # Filtered species: Only eucalyptus
```

```
##   site_location_name veg_barcode
## 1         NTAMGD0003   NTA018666
## 2         NTASTU0003   NTA017292
## 3         NTASTU0004   NTA017646
## 4         SASMDD0008   SAS001838
## 5         SASMDD0008   SAS001782
## 6         WAACOO0022 WAA  001863
##                         herbarium_determination is_uncertain_determination
## 1                         Eucalyptus tetrodonta                      FALSE
## 2                         Eucalyptus patellaris                      FALSE
## 3                          Eucalyptus tectifica                      FALSE
## 4 Eucalyptus camaldulensis subsp. camaldulensis                      FALSE
## 5                       Eucalyptus largiflorens                      FALSE
## 6   Eucalyptus celastroides subsp. celastroides                      FALSE
##      visit_start_date site_location_visit_id primary_gen_barcode
## 1 2016-04-28T09:38:07                  58431                <NA>
## 2 2016-05-01T15:10:00                  58430           NTA017293
## 3 2016-05-03T09:41:51                  58426           NTA017647
## 4 2015-04-26T08:29:02                  57638           SAS001839
## 5 2015-04-26T08:29:02                  57638           SAS001783
## 6 2013-11-01T16:06:00                  53453         WAA  001864
##   secondary_gen_barcode_1 secondary_gen_barcode_2 secondary_gen_barcode_3
## 1                    <NA>                    <NA>                    <NA>
## 2                    <NA>                    <NA>                    <NA>
## 3                    <NA>                    <NA>                    <NA>
## 4               SAS001841               SAS001840               SAS001842
## 5               SAS001784               SAS001785               SAS001786
## 6             WAA  001868             WAA  001867             WAA  001866
##   secondary_gen_barcode_4      site_unique
## 1                    <NA> NTAMGD0003-58431
## 2                    <NA> NTASTU0003-58430
## 3                    <NA> NTASTU0004-58426
## 4                    <NA> SASMDD0008-57638
## 5               SAS001787 SASMDD0008-57638
## 6             WAA  001865 WAACOO0022-53453
```

```
head(AP.data$veg.PI)  # Unfiltered species
```

```
##   site_location_name site_location_visit_id transect point_number
## 1         NSACOP0001                  58551    N3-S3           94
## 2         NSACOP0001                  58551    N3-S3           95
## 3         QDACYP0008                  58593    N4-S4           71
## 4         QDACYP0006                  58591    E5-W5            0
## 5         QDACYP0006                  58591    E5-W5            1
## 6         QDACYP0006                  58591    E5-W5            1
##   veg_barcode herbarium_determination substrate in_canopy_sky  dead
## 1   NSA013993      Geijera parviflora    Litter         FALSE FALSE
## 2   NSA013993      Geijera parviflora    Litter          TRUE FALSE
## 3        <NA>                    <NA>      Bare            NA    NA
## 4        <NA>                    <NA>    Litter            NA    NA
## 5   QDA015345  Crotalaria medicaginea    Litter         FALSE FALSE
## 6   QDA015601 Schizachyrium perplexum    Litter         FALSE FALSE
##     growth_form height hits_unique      site_unique
## 1     Tree/Palm   5.00    N3-S3 94 NSACOP0001-58551
## 2     Tree/Palm     NA    N3-S3 95 NSACOP0001-58551
## 3          <NA>     NA    N4-S4 71 QDACYP0008-58593
## 4          <NA>     NA     E5-W5 0 QDACYP0006-58591
## 5          Forb   0.25     E5-W5 1 QDACYP0006-58591
## 6 Tussock grass   0.10     E5-W5 1 QDACYP0006-58591
```

```
head(AP.data$veg.basal)  # Unfiltered species
```

```
##   site_location_name site_location_visit_id site_location_id point_id
## 1         NTASTU0003                  58430            61139       SW
## 2         NTASTU0003                  58430            61139        E
## 3         NTASTU0003                  58430            61139        W
## 4         NTASTU0003                  58430            61139       NE
## 5         NTASTU0003                  58430            61139       NW
## 6         NSAMDD0007                  56970            60231       NW
##   herbarium_determination veg_barcode hits basal_area_factor basal_area
## 1 Corymbia dichromophloia   NTA012918    3               0.1        0.3
## 2 Corymbia dichromophloia   NTA012918    4               0.1        0.4
## 3 Corymbia dichromophloia   NTA012918    3               0.1        0.3
## 4 Corymbia dichromophloia   NTA012918    2               0.1        0.2
## 5 Corymbia dichromophloia   NTA012918    1               0.1        0.1
## 6   Eucalyptus incrassata  NSA 010547    2               0.1        0.2
##        site_unique
## 1 NTASTU0003-58430
## 2 NTASTU0003-58430
## 3 NTASTU0003-58430
## 4 NTASTU0003-58430
## 5 NTASTU0003-58430
## 6 NSAMDD0007-56970
```

```
head(AP.data$struct.summ)  # Unfiltered species
```

```
##   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 1.124863 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] 624  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 oleosa 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
```

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

```
## [1] 685871     13
```

```
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"
```

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

```
##   site_location_name site_location_visit_id transect point_number
## 1         QDACYP0002                  58586    N5-S5            0
## 2         QDACYP0002                  58586    N5-S5            1
## 3         QDACYP0002                  58586    N5-S5            2
## 4         QDACYP0002                  58586    N5-S5            2
## 5         QDACYP0002                  58586    N5-S5            3
## 6         QDACYP0002                  58586    N5-S5            3
##   veg_barcode                herbarium_determination substrate
## 1 QDA  008105 Melaleuca viridiflora var. viridiflora      Bare
## 2 QDA  008115              Asteromyrtus lysicephala    Litter
## 3 QDA  008115              Asteromyrtus lysicephala    Litter
## 4 QDA  008149                     Schoenus sparteus    Litter
## 5 QDA  008115              Asteromyrtus lysicephala    Crypto
## 6   QDA012137                    Drosera petiolaris    Crypto
##   in_canopy_sky  dead growth_form height hits_unique      site_unique
## 1         FALSE FALSE       Shrub   1.30     N5-S5 0 QDACYP0002-58586
## 2         FALSE FALSE       Shrub   0.91     N5-S5 1 QDACYP0002-58586
## 3         FALSE FALSE       Shrub   1.30     N5-S5 2 QDACYP0002-58586
## 4         FALSE FALSE       Sedge   0.32     N5-S5 2 QDACYP0002-58586
## 5         FALSE FALSE       Shrub   0.58     N5-S5 3 QDACYP0002-58586
## 6         FALSE FALSE        Forb   0.01     N5-S5 3 QDACYP0002-58586
```

MANIPULATING AusPlots DATA

The retrieved data by the function 'get_ausplots' can be manipulated as any other R data. However, the 'deep' structure of the data (a list of multiple data frames) and interrelation of the data frames (via a common a common link variable) can make manipulating the data a bit more daunting.

As an example, we will focus on the sites in the 5 most sampled Bioregions. We will first identify which are these regions, and then subset the sites in these regions.

```
#-------------------------------------------------------------------------------------
# Find the 5 most 'sampled' Bioregions
#-------------------------------------------------------------------------------------

# Create a derived Bioregions Factor Variable in the 'site.info' DF
AP.data$site.info$bioregion.f = factor(AP.data$site.info$bioregion_name)
#names(AP.data$site.info)

# Display the Bioregions number of visits (from most visited to least visited)
sort(summary(AP.data$site.info$bioregion.f), decreasing=TRUE)
```

```
## MDD SSD GFU STP PIL FLB MGD GUP COO RIV BHC MAC FIN AUA CHC NUL CYP SYB
##  52  48  41  38  35  34  34  33  32  32  30  28  18  15  13  13  10   9
## EIU MUL BRT HAM MUR STU GVD AVW KAN SWA VIB ARP CEK DAC DMR EYB GAW GES
##   7   7   6   6   6   6   5   4   4   4   4   3   3   3   3   3   3   3
## JAF LSD MAL NSS PCK BBS COP GAS MII NAN DAB DAL ESP GSD
##   3   3   3   3   3   2   2   2   2   2   1   1   1   1
```

```
# Get the Names of the 5 most visited Bioregions
Bioregs.Top5.s = names(sort(summary(AP.data$site.info$bioregion.f), decreasing=TRUE)[1:5])
Bioregs.Top5.s
```

```
## [1] "MDD" "SSD" "GFU" "STP" "PIL"
```

```
#-------------------------------------------------------------------------------------
# Subset data for the 5 most 'visited/sampled' Bioregions
#-------------------------------------------------------------------------------------

summary(AP.data)
```

```
##           Length Class      Mode
## site.info 44     data.frame list
## veg.basal 10     data.frame list
## veg.PI    13     data.frame list
## citation   1     -none-     character
```

```
# Subset the 5 most sampled Bioregions in the 'site.info' data frame
# ================================================================
dim(AP.data$site.info)
```

```
## [1] 624  44
```

```
AP.BioregTop5.l = AP.data
AP.BioregTop5.l$site.info = AP.BioregTop5.l$site.info[AP.BioregTop5.l$site.info$bioregion_nam
e %in% Bioregs.Top5.s, ]
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Drop unused levels in the bioregion.f factor (i.e. the levels corresponding to other
# bioregions are dropped).
levels(AP.BioregTop5.l$site.info$bioregion.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"
```

```
AP.BioregTop5.l$site.info$bioregion.f = droplevels(AP.BioregTop5.l$site.info$bioregion.f)
levels(AP.BioregTop5.l$site.info$bioregion.f)
```

```
## [1] "GFU" "MDD" "PIL" "SSD" "STP"
```

```
# Subset the 5 most sampled Bioregions in the 'veg.PI' data frame
# ================================================================
# Because we are just subsetting the sites within the 5 most
# sampled bioregions, using the variable 'site_location_name'
# is enough (i.e. we don't need to use the variable 'site_unique').
dim(AP.BioregTop5.l$veg.PI)
```

```
## [1] 685871     13
```

```
AP.BioregTop5.l$veg.PI = AP.BioregTop5.l$veg.PI[AP.BioregTop5.l$veg.PI$site_location_name %in
% AP.BioregTop5.l$site.info$site_location_name, ]
dim(AP.BioregTop5.l$veg.PI)
```

```
## [1] 225242     13
```

```
# Subset the 5 most sampled Bioregions in the 'veg.basal' data frame
# ==================================================================
# Because we are just subsetting the sites within the 5 most
# sampled bioregions, using the variable 'site_location_name'
# is enough (i.e. we don't need to use the variable 'site_unique').
dim(AP.BioregTop5.l$veg.basal)
```

```
## [1] 7661   10
```

```
AP.BioregTop5.l$veg.basal = AP.BioregTop5.l$veg.basal[AP.BioregTop5.l$veg.basal$site_location
_name %in% AP.BioregTop5.l$site.info$site_location_name, ]
dim(AP.BioregTop5.l$veg.basal)
```

```
## [1] 2038   10
```

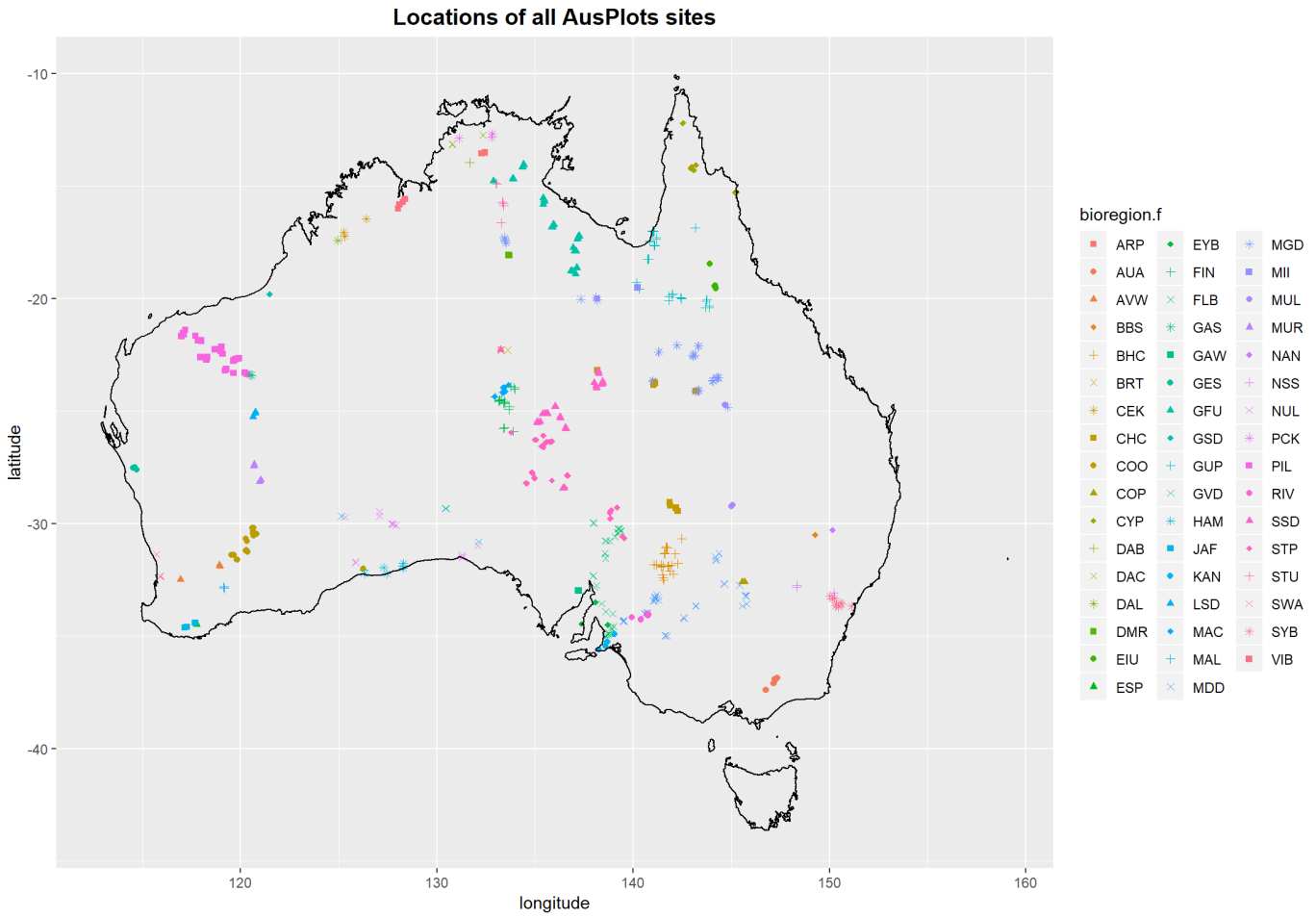
MAP THE SITES

Next we visualise the sites on a map of Australia. First we graph all the Sites curently in AusPlots and then the Sites in the 5 most sampled bioregions. To do so we first obtain the map from the `maps` package and convert it to `SpatialPolygons`. Then we plot the Sites on the SpatialPolygon object for the map of Australia using functions in the `ggplot2` package. To differenciate among bioregions, sites are represented by different shapes and colours in the first graph, and by dots of different colours in the second one.

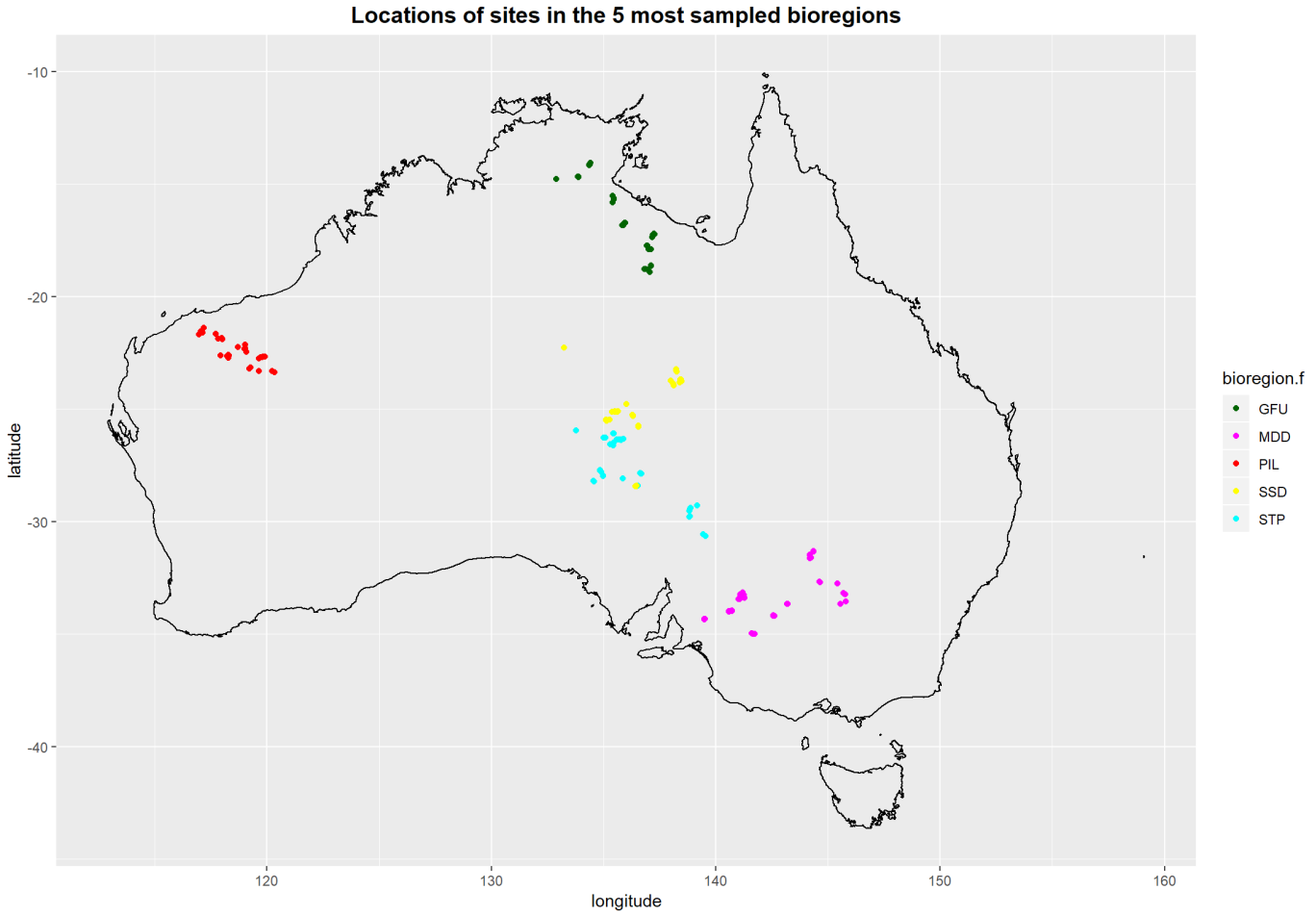
```
#-------------------------------------------------------------------------------------------
# Get and Prepare a Map of Australia
#-------------------------------------------------------------------------------------------

# Maps in the package 'maps' are projected in longlat by default
aus = map("worldHires", "Australia", fill=TRUE, xlim=c(110,160),ylim=c(-45,-5), mar=c(0,0,0,0
), plot=FALSE)

# Convert map data to SpatialPolygons
#aus.sp = map2SpatialPolygons(aus, IDs=aus$names, proj4string=CRS("+proj=longlat"))
CRS("+init=epsg:4326") # More info (i.e. provides a datum)
```

```
## CRS arguments:
##  +init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84
## +towgs84=0,0,0
```

```
aus.sp = map2SpatialPolygons(aus, IDs=aus$names, proj4string=CRS("+init=epsg:4326"))


#-------------------------------------------------------------------------------------
# Plot All AusPlots Sites on a Map of Australia
#-------------------------------------------------------------------------------------

# We well use 7 distinct symbol shapes to represent the AusPlots Sites (combined with
# different colors). We will cycle through the 7 symbol shapes. We start by creating a
# vector of with symbol shapes codes as long as the number of bioregions in the current
# version of the AusPlots dataset, cycling among the 7 shapes. What complicates this
# process a bit is that the number of bioregions sampled changes with time, as additional
# sites in different bioregions are sampled. Thus, we need to estimate the required number
# of cycles of symbol shapes from the data. To do this we use the function ceiling, and
# the cut back to the required number of symbol shapes as we might not need full cycles
# (i.e. the number of sites might not be a multiple of 7; e.g. 50 sites require more than
# 7 cycles, so we use 8 and then trimm the vector from 56 (7 shapes * 8 cycles) to 50.

# Preparation: Create a vector with the symbol shapes values
bioregions.cnt = length(levels(AP.data$site.info$bioregion.f))
shape.cycles.num = ceiling(bioregions.cnt / 7) #  Using 7 distinct Symbol Shapes
sites.shape.values = rep(c(15:18,3:4,8),shape.cycles.num)[1:bioregions.cnt]

# Create Plot
ggplot( data=AP.data$site.info,
             aes(x = longitude, y = latitude, group=bioregion.f), alpha =0.5) +
geom_point(aes(colour=bioregion.f, fill=bioregion.f, shape=bioregion.f), size=1.5) +
scale_shape_manual(values=sites.shape.values) +  # Cycle through Symbol Types
ggtitle("Locations of all AusPlots sites") +
theme(plot.title = element_text(hjust = 0.5, face="bold", size=14)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)
```




```
#-----------------------------------------------------------------------------------------
# Plot AusPlots sites in the 5 Bioregions on Map of Australia
#-----------------------------------------------------------------------------------------
ggplot(data=AP.BioregTop5.l$site.info, aes(x = longitude, y = latitude, colour=bioregion.f, f
ill=bioregion.f), alpha =0.5) +
geom_point(pch=21, size=1.5) + scale_colour_manual(values = c("darkgreen", "magenta", "red",
"yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
ggtitle("Locations of sites in the 5 most sampled bioregions") +
theme(plot.title = element_text(hjust = 0.5, face="bold", size=14)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)
```



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

In this section, we will explore to how to obtain and use species occurrence data from AusPlots raw data. In particular, we will examine species cover/abundance, species presence/absence, multiple indices of species diversity, and rank-abundance plots for the sites in the 5 most sampled bioregions.

First step: Create a species occurence matrix

The first step to work with species-level AusPlots data is to create a species occurrence matrix. The `species_table` function in the `ausplotsR` package can be used to effortlessly create this type of matrix. This 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* (argument `m_kind = PA`).
- *Percent Cover*: Based on total frequency of hits. This is the most commonly used metric (argument `m_kind = percent_cover`).
- *Frequency*: Based on proportional frequencies of presence on the 10 individual transects within a plot (argument `m_kind = freq`). It can be a measure of importance for low cover species.
- *IVI*: A combination of cover and frequency (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 (argument `cover_type = PFC`).
- *Opaque Canopy Cover* (*OCC*): Hits scored as 'in canopy sky' are retained (argument `cover_type = OCC`).

```
# Use function 'species_table' in 'ausplotsR' package to create an Abundance per Site Table
# ============================================================================================
SppBYSites.BioregTop5 = species_table(AP.BioregTop5.l$veg.PI, m_kind="percent_cover", cover_t
ype="PFC")
class(SppBYSites.BioregTop5)
```

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

```
dim(SppBYSites.BioregTop5) # Number of rows and columns in the matrix: 574 Sites x 3024 Spp
```

```
## [1]  210 1093
```

```
SppBYSites.BioregTop5[1:5, 1:5]
```

```
##                  Abutilon.fraseri Abutilon.halophilum Abutilon.otocarpum
## NSAMDD0001-56965                0                   0                  0
## NSAMDD0002-56952                0                   0                  0
## NSAMDD0003-56968                0                   0                  0
## NSAMDD0004-56953                0                   0                  0
## NSAMDD0005-56969                0                   0                  0
##                  Abutilon.oxycarpum Abutilon.sp.
## NSAMDD0001-56965                  0            0
## NSAMDD0002-56952                  0            0
## NSAMDD0003-56968                  0            0
## NSAMDD0004-56953                  0            0
## NSAMDD0005-56969                  0            0
```

```
# Enrich Table with: Site_Location, Bioregion, Latitude, and Longitude
# ====================================================================

# Create a 'site_unique' variable in Species by Sites Table to relate both datasets
# ----------------------------------------------------------------------------------
SppBYSites.BioregTop5$site_unique = rownames(SppBYSites.BioregTop5)

# Both DF have differente number of rows!
dim(SppBYSites.BioregTop5)
```

```
## [1]  210 1094
```

```
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
# -----------------------------------------------
SppBYSites.BioregTop5  = merge(SppBYSites.BioregTop5, AP.BioregTop5.l$site.info,
by="site_unique")[,c(names(SppBYSites.BioregTop5),
                                          "bioregion.f", "longitude", "latitude")]
SppBYSites.BioregTop5 = na.omit(SppBYSites.BioregTop5)
#head(SppBYSites.BioregTop5)
#summary(SppBYSites.BioregTop5)
head(names(SppBYSites.BioregTop5))
```

```
## [1] "Abutilon.fraseri"    "Abutilon.halophilum" "Abutilon.otocarpum"
## [4] "Abutilon.oxycarpum"  "Abutilon.sp."        "Acacia.adoxa"
```

Species Abundance

In AusPlots data percent cover is used as a measure of abundance. In this section, we will examine percent cover by:

- Site visit and species: That is, all cells in the 'Species by Sites' table.
- Species: By computing the column totals in the 'Species by Sites' table.

Percent Cover (Abundance) by Site Visit x Species

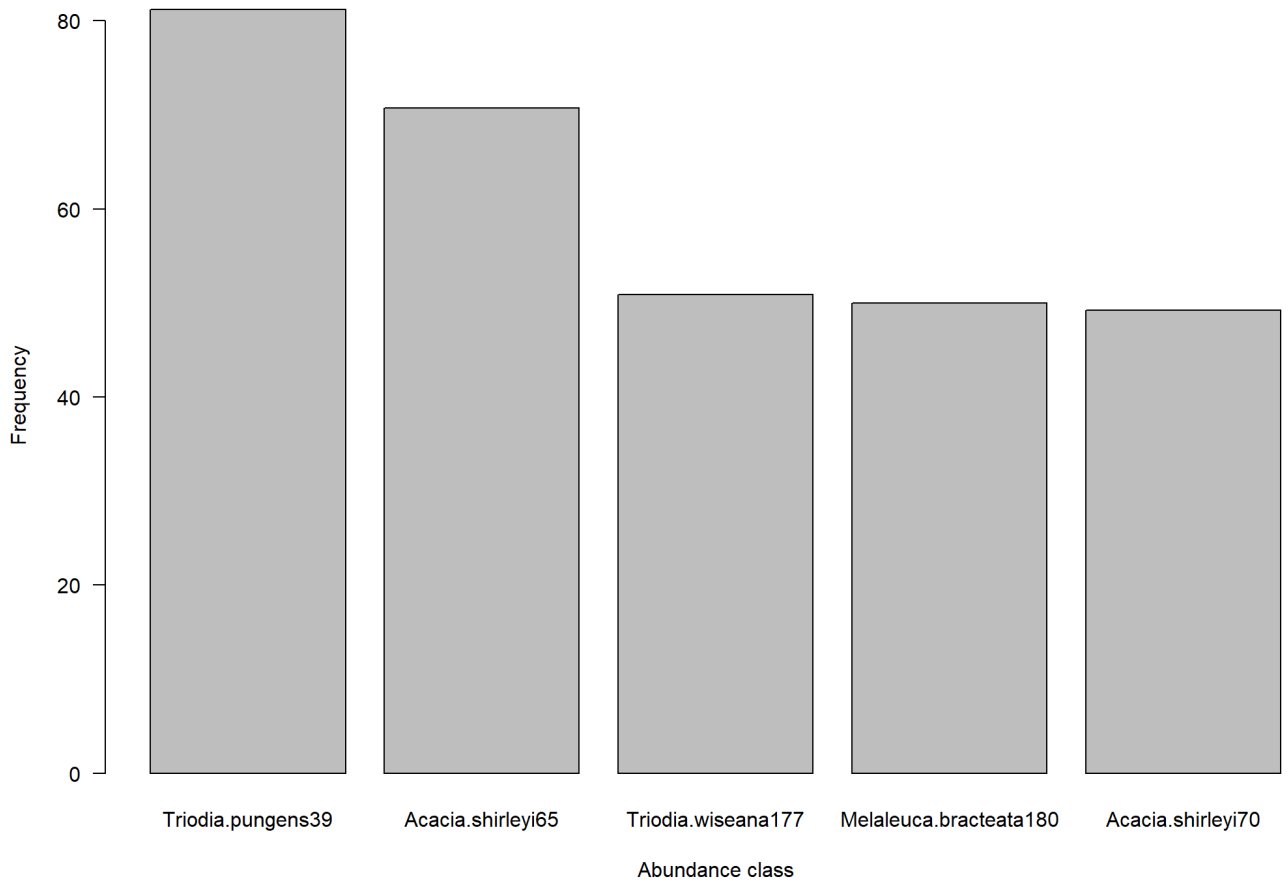
```
# Minimum and Maximum Site Visit x Species Abundance values
# ---------------------------------------------------------
# '-4' because we added 4 new columns (Plot, bioregion.f, longitude, and latitude)##
range(SppBYSites.BioregTop5[,1: (dim(SppBYSites.BioregTop5)[2]-4)])
```

```
## [1]  0.00000 81.18812
```

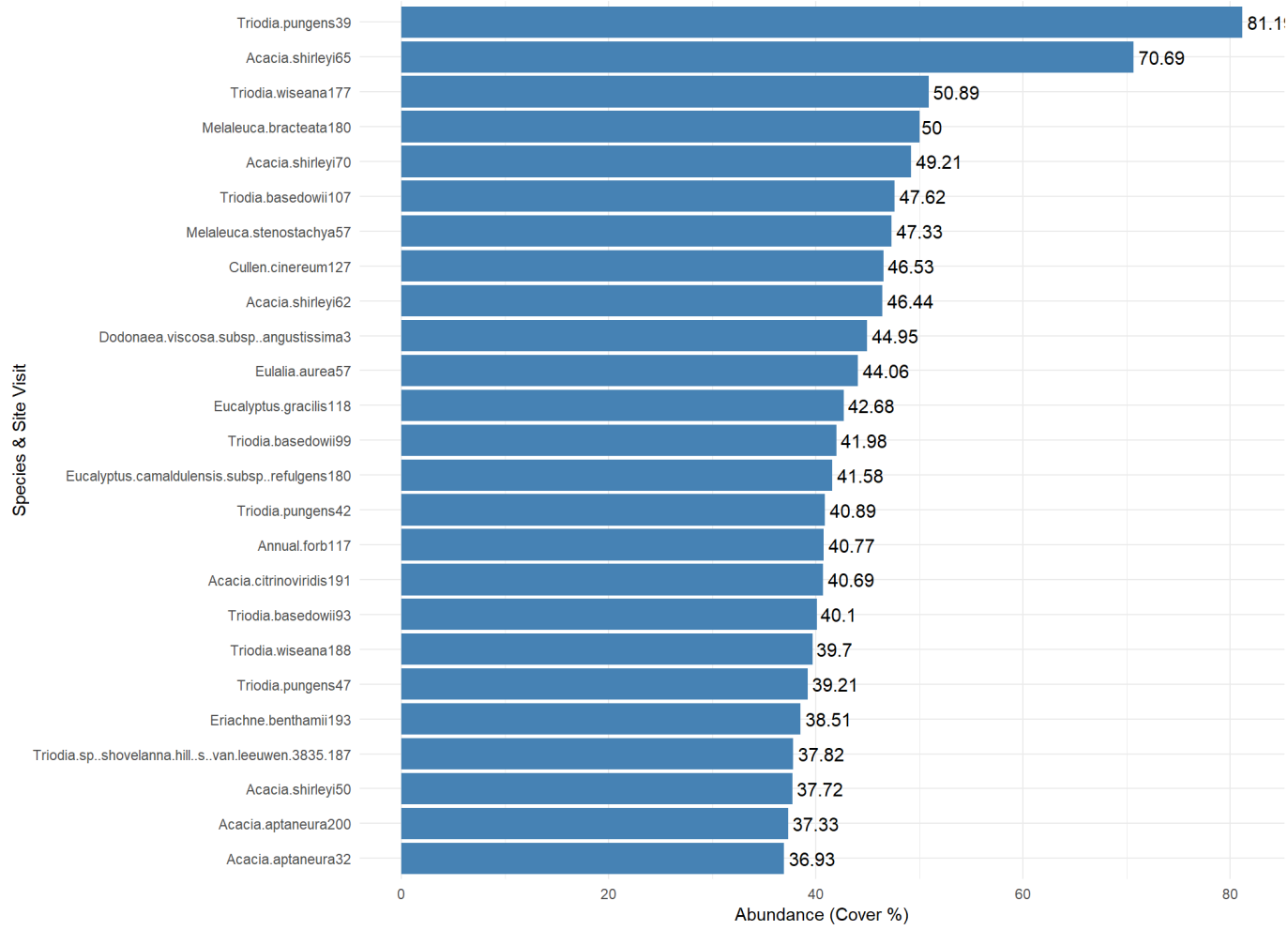
```
# Plot Highest  Site Visit x Species Abundance values
# ----------------------------------------------------
Abundance = unlist(SppBYSites.BioregTop5[,1: (dim(SppBYSites.BioregTop5)[2]-4)])
head(Abundance)
```

```
## Abutilon.fraseri1 Abutilon.fraseri2 Abutilon.fraseri3 Abutilon.fraseri4
##                 0                 0                 0                 0
## Abutilon.fraseri5 Abutilon.fraseri6
##                 0                 0
```

```
#length(Abundance)
#dim(SppBYSites.BioregTop5)

# Plot the 5 Site Visits x Species combination with the Highest Abundances
par(mfrow=c(1,1))
barplot(sort(Abundance, decreasing=TRUE)[1:5], las=1, xlab="Abundance class", ylab="Frequenc
y")
```




```
# ggplot2 graph to make it look nicer. Now we plot the 25 species-site visit covers with hori
zontal bars
temp.labs = names(sort(Abundance, decreasing=TRUE))
temp.Abundances = sort(Abundance, decreasing=TRUE)
temp.df = data.frame(temp.Abundances, temp.labs)
# Order factor levels so that bars are sorted by Abundance in the plot. Otherwise they would
 plotted in alphabetical order
# 'rev' to plot bars in decreasing order (i.e. larger bar at top; otherwise larger bar at bot
tom)
temp.df$temp.labs = factor(temp.df$temp.labs, levels=rev(temp.df$temp.labs))
ggplot(data=temp.df[1:25,], aes(x=temp.labs, y=temp.Abundances)) +
geom_bar(stat="identity", fill="steelblue") +
geom_text(aes(label=round(temp.Abundances,2)), hjust=-0.1, size=4)+
labs(x="Species & Site Visit", y="Abundance (Cover %)") +
theme_minimal() + coord_flip()
```




```
# Cleaning up
rm(list=ls(pattern="temp."))
```

Abundance (Cover %) by Species

Now we compute the percent cover of all species across the sites in the 5 most sampled bioregions. Then we find and plot on a map of Australia the 4 most Abundant species in the 5 regions (across all regions pooled together).

```
# Compute Species Total Abundance (Cover %)
# -----------------------------------------
TotAbundances.BioregTop5 = colSums(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4
)])
head(TotAbundances.BioregTop5)
```

```
##    Abutilon.fraseri Abutilon.halophilum  Abutilon.otocarpum
##           0.2970297           1.2871287           2.5757352
##  Abutilon.oxycarpum        Abutilon.sp.        Acacia.adoxa
##           0.3960396           0.5944519           0.4950495
```

```
# Species with Highest Total Abundance
# ------------------------------------
# Species with Highest Total Abundance
max(TotAbundances.BioregTop5)
```

```
## [1] 366.8182
```

```
which.max(TotAbundances.BioregTop5)
```

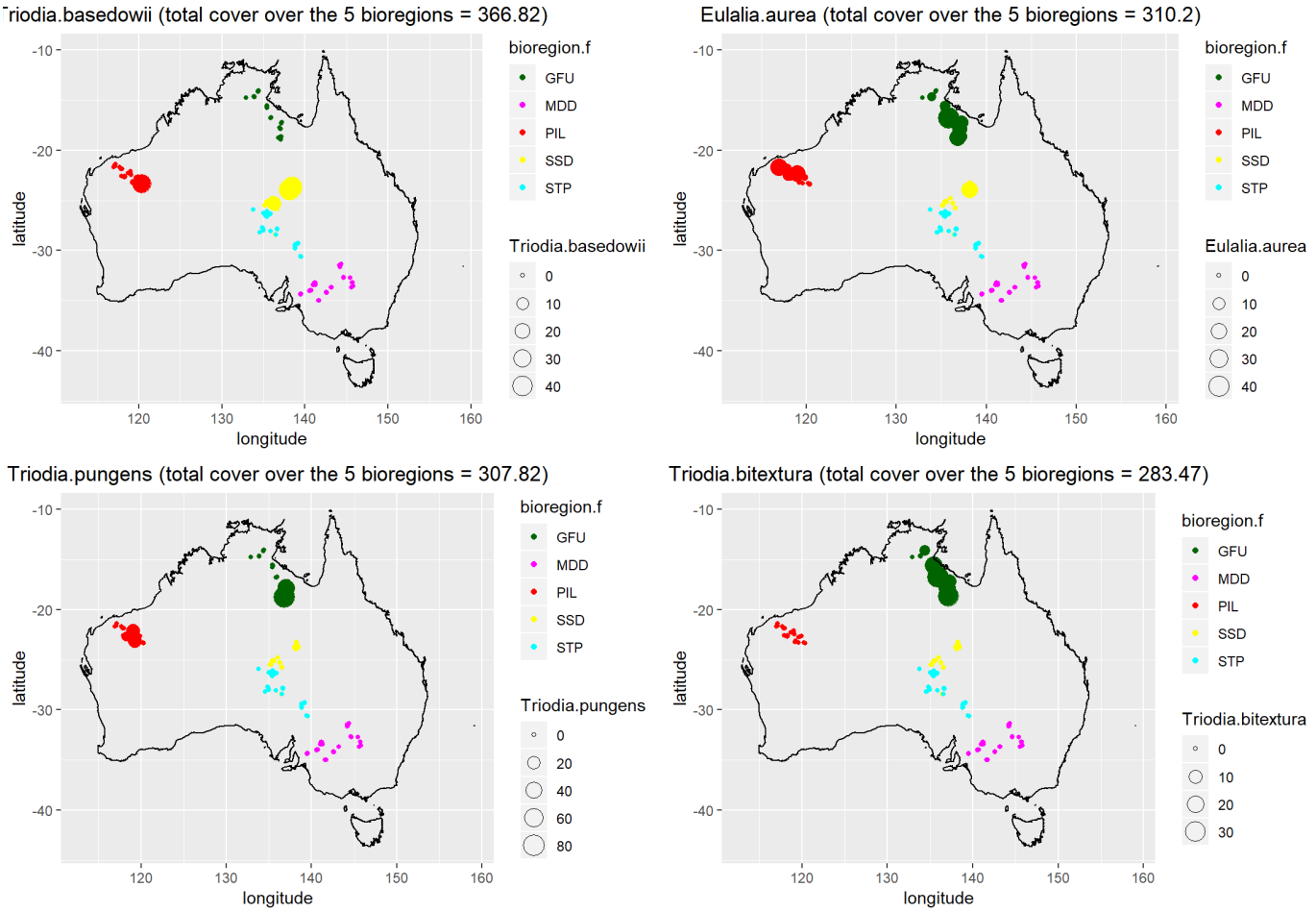
```
## Triodia.basedowii
##              1035
```

```
# Species with Top 4 Highest Abundances
TotAbundances4Highest.indices =
     which(TotAbundances.BioregTop5 >= sort(TotAbundances.BioregTop5, decreasing=T)[4],
arr.ind=T)
sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices], decreasing=TRUE)
```

```
## Triodia.basedowii     Eulalia.aurea   Triodia.pungens Triodia.bitextura
##          366.8182          310.1988          307.8218          283.4677
```

```
# Plot 4 Species with Highest Cover in the 5 Most Sampled Bioregions
# ------------------------------------------------------------------

# Most Abundant Species
spp = names(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE))[1]
plot.title =  paste(spp, " (total cover over the 5 bioregions = ",
                    round(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE)[1],2) , ")", sep="")
TotAbundance.spp1 =
ggplot(data=SppBYSites.BioregTop5, aes(x=longitude, y=latitude, colour=bioregion.f, fill=bior
egion.f), alpha =0.5) +
geom_point(aes_string(size=spp), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
ggtitle(plot.title) + theme(plot.title = element_text(hjust = 0.5)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# 2nd Most Abundant Species
spp = names(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE))[2]
plot.title =  paste(spp, " (total cover over the 5 bioregions = ",
                    round(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE)[2],2) , ")", sep="")
TotAbundance.spp2 =
ggplot(data=SppBYSites.BioregTop5, aes(x=longitude, y=latitude, colour=bioregion.f, fill=bior
egion.f), alpha =0.5) +
geom_point(aes_string(size=spp), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
ggtitle(plot.title) + theme(plot.title = element_text(hjust = 0.5)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# 3rd Most Abundant Species
spp = names(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE))[3]
plot.title =  paste(spp, " (total cover over the 5 bioregions = ",
                    round(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE)[3],2) , ")", sep="")
TotAbundance.spp3 =
ggplot(data=SppBYSites.BioregTop5, aes(x=longitude, y=latitude, colour=bioregion.f, fill=bior
egion.f), alpha =0.5) +
geom_point(aes_string(size=spp), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
ggtitle(plot.title) + theme(plot.title = element_text(hjust = 0.5)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# 4th Most Abundant Species
spp = names(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE))[4]
plot.title =  paste(spp, " (total cover over the 5 bioregions = ",
                    round(sort(TotAbundances.BioregTop5[TotAbundances4Highest.indices],
decreasing=TRUE)[4],2) , ")", sep="")
TotAbundance.spp4 =
ggplot(data=SppBYSites.BioregTop5, aes(x=longitude, y=latitude, colour=bioregion.f, fill=bior
egion.f), alpha =0.5) +
```

```
geom_point(aes_string(size=spp), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
ggtitle(plot.title) + theme(plot.title = element_text(hjust = 0.5)) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# Plot the 4 Graphs
grid.arrange(TotAbundance.spp1, TotAbundance.spp2, TotAbundance.spp3, TotAbundance.spp4, nrow
=2)
```



Species Occurrence (Presence/Absence)

We next focus on species occurrence data; that is, whether as species is Present/Absent. We can compute Presence/Absence data in several ways:

- Re-use the 'percent cover' data we used above: If percent cover is > 0 then the species is present, if percent cover = 0 then the species is absent.
- Use the `species_table` function with the argument `m_kind = PA` on the data frame with raw point intercept data (i.e. `veg.PI`) generated by the function `get_auplots` .
- Use the `species_table` function with the argument `m_kind = PA` on the data frame with vegetation vouchers data (a complete set of species records for the plot determined by a herbarium; i.e. `veg.vouchers`) generated by the function `get_auplots` . This option provides the most complete species inventories by sites.

Here we use the first option for simplicity and generality (i.e. how these tasks can be performed with other abundance data outside AusPlots). As for the Abundance/Percent Cover data, we first examine species occurrence across all cells (i.e. combinations of site visits and species), and then investigate and plot the total number of (absolute and relative) occurrences for each species.

```
# Presence/Absence across all Cells (i.e. Site Visit x Species)
# ============================================================

# Absolute Presences/Absences
# ---------------------------
 # Number of Presences
sum(Abundance > 0)
```

```
## [1] 4035
```

```
 # Number of Absences
sum(Abundance == 0)
```

```
## [1] 225495
```

```
# Relative (%) Presences/Absences
# -------------------------------
num.cells = (nrow(SppBYSites.BioregTop5[1: (dim(SppBYSites.BioregTop5)[1]-3)]) * ncol(SppBYSi
tes.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)]))
 # % of Presences
sum(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)] > 0)/ num.cells
```

```
## [1] 0.0175794
```

```
 # % of Absences
sum(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)] == 0) / num.cells
```

```
## [1] 0.9824206
```

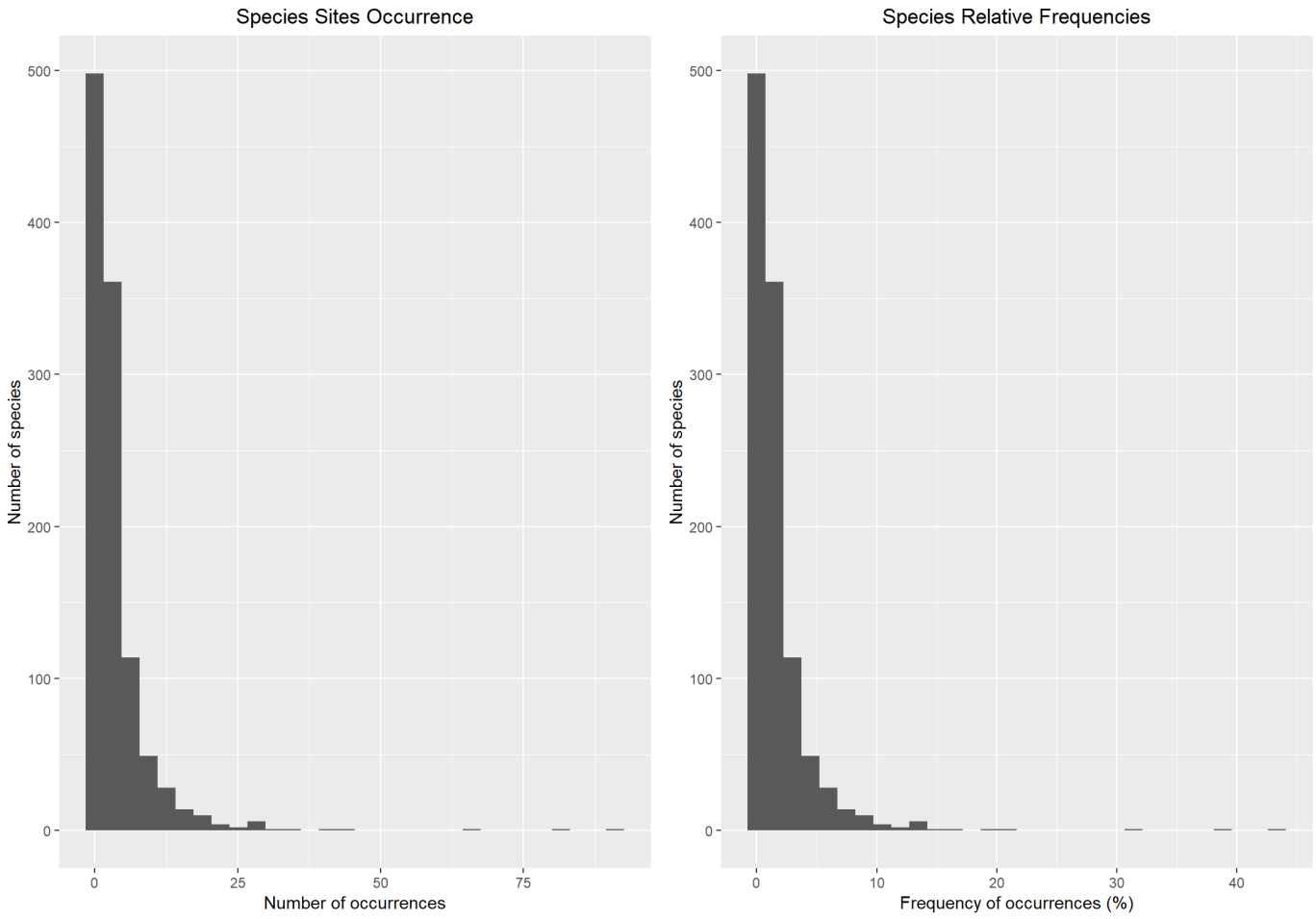
```
# Total Presence/Absence  for each Species (i.e. per data frame Column)
# ======================================================================

# Compute number of sites where each species is present (sum by columns)
head(names(SppBYSites.BioregTop5)) # Species are in columns
```

```
## [1] "Abutilon.fraseri"    "Abutilon.halophilum" "Abutilon.otocarpum"
## [4] "Abutilon.oxycarpum"  "Abutilon.sp."        "Acacia.adoxa"
```

```
SppPres.BioregTop5 = apply(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)]>0, 2,s
um)

# Sort results in increasing order
head(sort(SppPres.BioregTop5, decreasing = TRUE))
```

```
##        Annual.forb       Annual.grass    Dead.tree.shrub
##                 92                 81                 65
##    Sida.fibulifera      Eulalia.aurea Aristida.holathera
##                 43                 40                 36
```

```
# Compute Percentage Frequencies
SppRelFreq.BioregTop5 =  SppPres.BioregTop5 * 100 / nrow(SppBYSites.BioregTop5)

# Plot Species Frequencies
par(mfrow=c(1,1))
spp.freq.p1 = ggplot() + geom_histogram(aes(SppPres.BioregTop5)) +
              ggtitle("Species Sites Occurrence") +
              theme(plot.title = element_text(hjust = 0.5)) +
              xlab("Number of occurrences") + ylab("Number of species")
spp.freq.p2 = ggplot() + geom_histogram(aes(SppRelFreq.BioregTop5)) +
              ggtitle("Species Relative Frequencies") +
              theme(plot.title = element_text(hjust = 0.5)) +
              xlab("Frequency of occurrences (%)") + ylab("Number of species")
grid.arrange(spp.freq.p1, spp.freq.p2, ncol=2)
```



Species Diversity

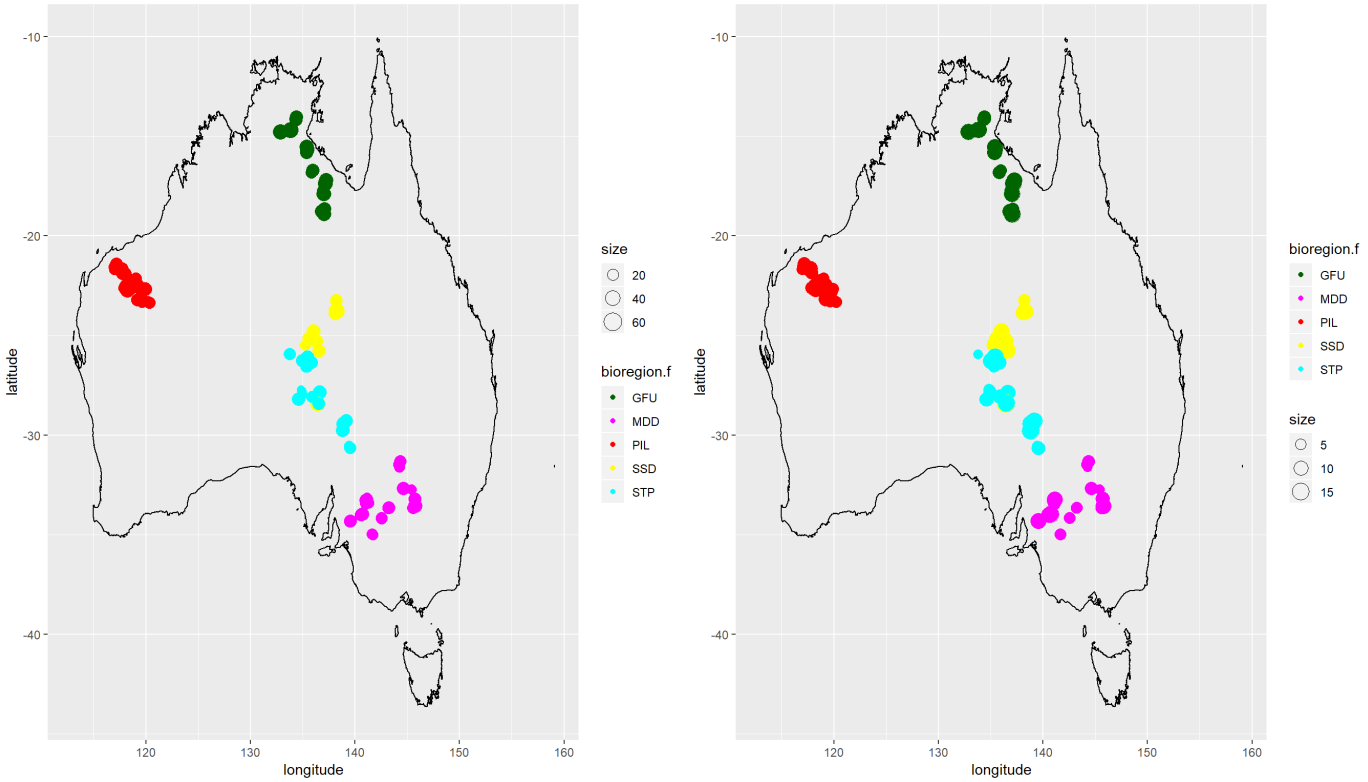
On our exploration of the use of Species-lelvel AusPlots data, we now focus on Species Diversity. We first compute 7 common diversity indices, which we then place in a dataset. Finally, as an example, we plot two of these indices (Species Richness and Shanon Diversity Index) for the sites in the 5 most sampled bioregions on a map of Australia.

NOTE: Diversity indices were originally designed to be used with counts of number of individuals per species, rather than percent cover, as a measure of abundance. These indices are also used with percent cover in the literature (see Tomasckik and Sander, 1987 for an example using coral cover). We need, however, to be aware of the different kind of answers and interpretation of the results required.

```
# Compute and place in a DF the Species Diversity Indices
# ======================================================

# Species Richness
N0 = rowSums(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)] > 0)
# Shannon Entropy
H = diversity(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)])
# Shannon Diversity Index
N1 = exp(H)
# Simpson Diversity Index
N2 = diversity(SppBYSites.BioregTop5[,1:(dim(SppBYSites.BioregTop5)[2]-4)], "inv")
# Shannon Evenness (Hill's ratio)
E1 = N1/N0
# Simpson Evenness (Hill's ratio)
E2 = N2/N0
# Pielou Evenness
J = H/log(N0)

# Create a Data Frame with the Species Diversity Indices
SppBYSites.BioregTop.Div.df = data.frame(N0, H, N1, N2, E1, E2, J)


# Map Species Richness and Shannon Diversity Index (as an example)
# ================================================================

# Add extra info to DataFrame (Bioregions, longitude, and latitude)
SppBYSites.BioregTop.Div.df$bioregion.f = SppBYSites.BioregTop5[rownames(SppBYSites.BioregTo
p.Div.df),"bioregion.f"]
SppBYSites.BioregTop.Div.df$longitude = SppBYSites.BioregTop5[rownames(SppBYSites.BioregTop.D
iv.df),"longitude"]
SppBYSites.BioregTop.Div.df$latitude = SppBYSites.BioregTop5[rownames(SppBYSites.BioregTop.Di
v.df),"latitude"]
summary(SppBYSites.BioregTop.Div.df)
```

```
##        N0              H               N1              N2
##  Min.   : 1.00   Min.   :0.000   Min.   : 1.000   Min.   : 1.000
##  1st Qu.:14.00   1st Qu.:1.403   1st Qu.: 4.067   1st Qu.: 2.768
##  Median :18.00   Median :1.779   Median : 5.923   Median : 4.110
##  Mean   :19.21   Mean   :1.780   Mean   : 6.926   Mean   : 4.638
##  3rd Qu.:24.00   3rd Qu.:2.185   3rd Qu.: 8.895   3rd Qu.: 5.768
##  Max.   :62.00   Max.   :2.866   Max.   :17.573   Max.   :13.797
##
##        E1               E2               J          bioregion.f
##  Min.   :0.08624   Min.   :0.05508   Min.   :0.1727   GFU:41
##  1st Qu.:0.26200   1st Qu.:0.16829   1st Qu.:0.5353   MDD:50
##  Median :0.34397   Median :0.23141   Median :0.6361   PIL:35
##  Mean   :0.37403   Mean   :0.26207   Mean   :0.6210   SSD:46
##  3rd Qu.:0.44665   3rd Qu.:0.30717   3rd Qu.:0.7179   STP:38
##  Max.   :1.00000   Max.   :1.00000   Max.   :0.9610
##                                      NA's   :1
##    longitude        latitude
##  Min.   :117.0   Min.   :-35.00
##  1st Qu.:134.9   1st Qu.:-29.78
##  Median :136.8   Median :-25.12
##  Mean   :134.9   Mean   :-25.38
##  3rd Qu.:139.2   3rd Qu.:-21.88
##  Max.   :145.8   Max.   :-14.05
##
```

```
# Create Species Richness Plot
Div.SR =
ggplot(data=SppBYSites.BioregTop.Div.df, aes(x=longitude, y=latitude, colour=bioregion.f, fil
l=bioregion.f), alpha =0.5) +
geom_point(aes_string(size=N0), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# Create Shanon Diversity Index Plot
Div.ShannonIndex =
ggplot(data=SppBYSites.BioregTop.Div.df, aes(x=longitude, y=latitude, colour=bioregion.f, fil
l=bioregion.f), alpha =0.5) +
geom_point(aes_string(size=N1), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# Plot the 2 graphs
grid.arrange(Div.SR, Div.ShannonIndex, ncol=2)
```



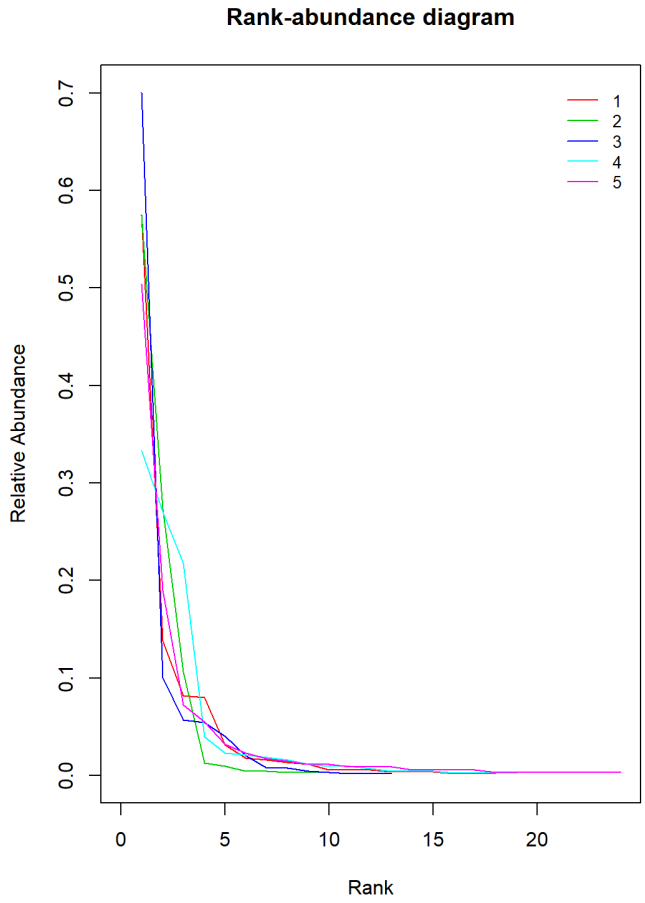
Rank-Abundance Curves & Relative Abundance Models

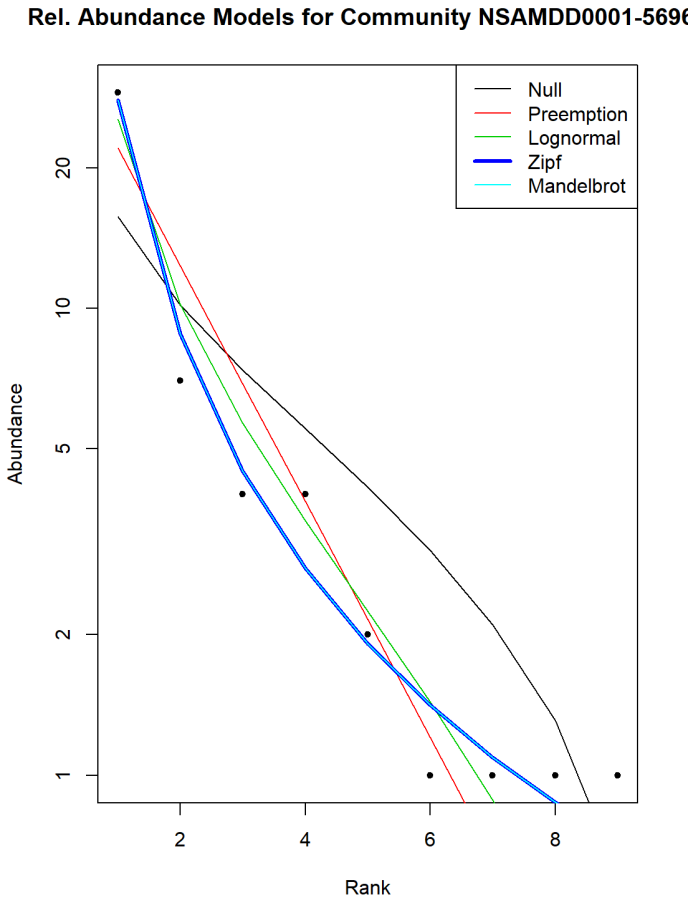
For the final example of downstream visualisation and analysis of Species-level AusPlots data, we focus on Rank-Abundance Curves (also known as Whittaker Plots). Rank-Abundance Curves provide further information on species diversity. They provide a more complete picture than a single diversity index. Their x-axis represents the abundance rank (from most to least abundant) and in the y-axis the species relative abundance. Thus, they depict both Species Richness (number of different in ranked) and Species Evenness (slope of the line that fits the rank; steep gradient indicates low evenness and a shallow gradient high evenness).

In this section we:

- We plot the Rank-Abundance Curves for the first 5 Site-Visits in our 5 most sampled bioregions dataset.
- We show a quick example of the fitting of possible Models of Relative Abundance for one Community.
- We compute the mean cover for each species in the 5 most sampled Bioregions and then plot the Rank-Abundance Curves for the 5 Bioregions.

```
par(mfrow=c(1,2))

# Rank-Abundance Curves (= Whittaker Plots) for the First 5 Site-Visits
# ======================================================================
goeveg::racurves(SppBYSites.BioregTop5[1:5,1:(dim(SppBYSites.BioregTop5)[2]-4)], bw=F)


# Possible Models of Relative Abundance for one Community
# =======================================================
plot(vegan::radfit(round(SppBYSites.BioregTop5[1,1:(dim(SppBYSites.BioregTop5)[2]-4)], digits
=0), log="xy"),
     pch=20, main="Rel. Abundance Models for Community NSAMDD0001-56965")
```





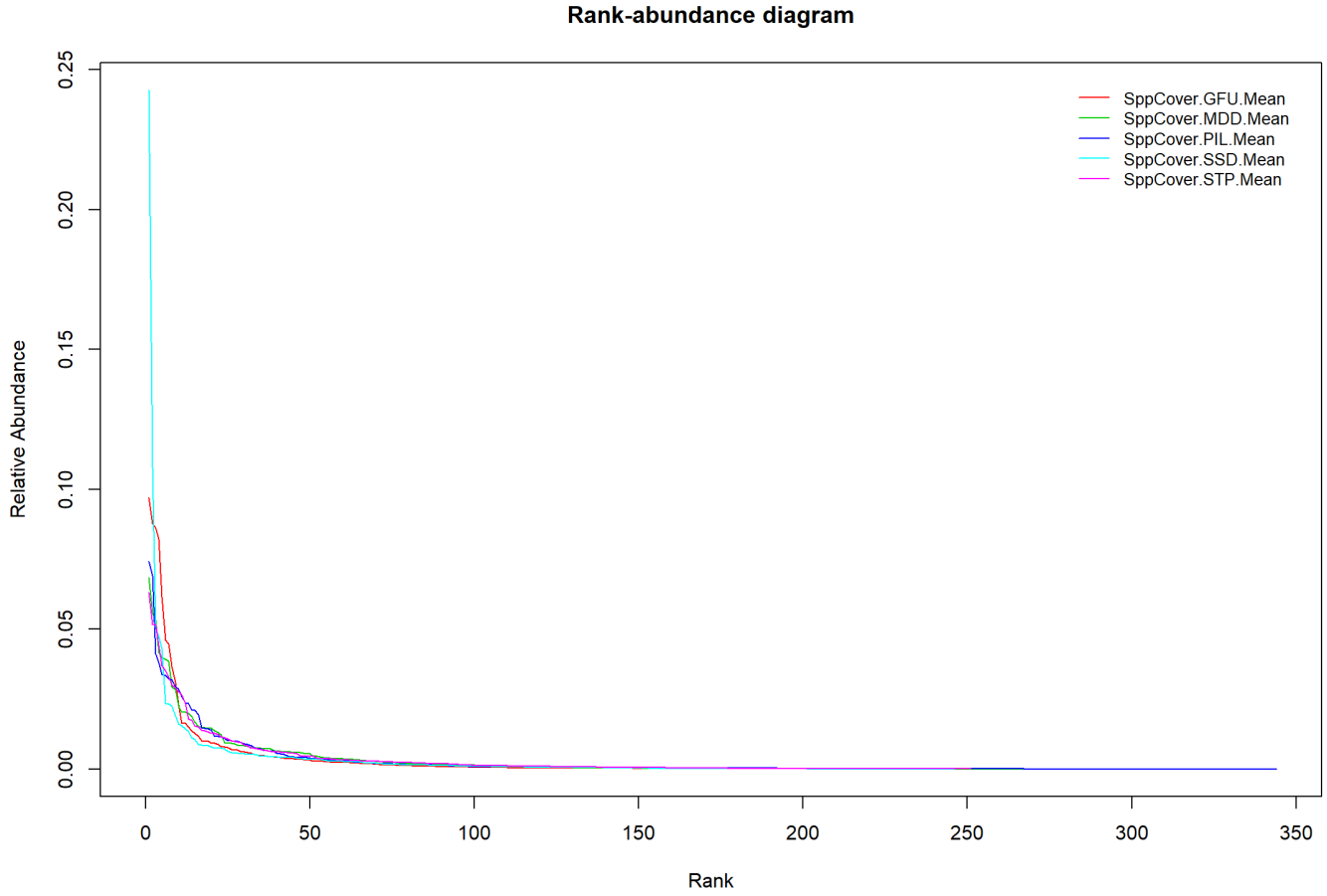

```
# Rank-Abundance Curves (= Whittaker Plots) for each Bioregion (using the Spp. Mean Cover)
# ==========================================================================================

# Compute Species Mean Cover for each of the 5 most sampled Bioregions
levels(SppBYSites.BioregTop5$bioregion.f)
```

```
## [1] "GFU" "MDD" "PIL" "SSD" "STP"
```

```
 # GFU
SppCover.GFU.Mean = apply(SppBYSites.BioregTop5[SppBYSites.BioregTop5$bioregion.f=="GFU",1:(d
im(SppBYSites.BioregTop5)[2]-4)], 2, mean)
#head(SppCover.GFU.Mean)
 # MDD
SppCover.MDD.Mean = apply(SppBYSites.BioregTop5[SppBYSites.BioregTop5$bioregion.f=="MDD",1:(d
im(SppBYSites.BioregTop5)[2]-4)], 2, mean)
#head(SppCover.MDD.Mean)
 # PIL
SppCover.PIL.Mean = apply(SppBYSites.BioregTop5[SppBYSites.BioregTop5$bioregion.f=="PIL",1:(d
im(SppBYSites.BioregTop5)[2]-4)], 2, mean)
#head(SppCover.PIL.Mean)
 # SSD
SppCover.SSD.Mean = apply(SppBYSites.BioregTop5[SppBYSites.BioregTop5$bioregion.f=="SSD",1:(d
im(SppBYSites.BioregTop5)[2]-4)], 2, mean)
#head(SppCover.SSD.Mean)
 # STP
SppCover.STP.Mean = apply(SppBYSites.BioregTop5[SppBYSites.BioregTop5$bioregion.f=="STP",1:(d
im(SppBYSites.BioregTop5)[2]-4)], 2, mean)
#head(SppCover.STP.Mean)

# Create a Matrix with Species Means per Bioregion
SppCover.BioregionMean.m = rbind(SppCover.GFU.Mean, SppCover.MDD.Mean, SppCover.PIL.Mean, Spp
Cover.SSD.Mean, SppCover.STP.Mean)
rownames(SppCover.BioregionMean.m)
```

```
## [1] "SppCover.GFU.Mean" "SppCover.MDD.Mean" "SppCover.PIL.Mean"
## [4] "SppCover.SSD.Mean" "SppCover.STP.Mean"
```

```
# Rank-Abundance Curves (= Whittaker Plots) for the Species Cover Mean in each of the 5 Biore
gions
par(mfrow=c(1,1))
goeveg::racurves(SppCover.BioregionMean.m, bw=F)
```



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

Fractional Cover (FC) is the proportional cover of green vegetation, dead vegetation and bare substrate, based on plot-based point intercept data from AusPlots (as generated by 'get_ausplots').

Cover fractions are assigned according to the following:

- '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 substrate that is rock, outcrop, gravel or bare soil with no veg cover.

A height rule is applied so that coding to green/brown/bare of the uppermost substrate/vegetation stratum hit at a given point intercept location overrides the others, that is, a dead tree overrides a living shrub beneath and vice versa; substrate coding is overridden by any vegetation cover etc. This means for each of the (usually) 1010 intercepts, there is a single coding and percentage is the number of hits assigned to each fraction, divided by the total number of PIs taken (usually 1010 but can vary) times 100.

There is an option via argument 'ground_fractional' to calculate fractional ground cover - the same concept applied to only 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.

'In canopy sky' is excluded by default (only the substrate is considered for those hits) and applies only to regular fractional cover (as trees are excluded in the green fraction for ground fractional cover by default).

Currently, cryptogam substrate is assigned to the non-photosynthetic fraction.

Occasionally substrate type was not collected ('NC') or could not be assigned to one of the above categories ('Unknwn'), in which case a percent cover will be returned under an 'NA' fraction if there was no veg cover above those points.

The function `fractional_cover` returns a data frame in which plots are rows, columns are fractions (bare, brown, green and NA) and values are percent cover.

In this section we will explore:

- The Latitudinal Pattern in Proportional Vegetation Cover (for a random subest of 200 sites).
- Temporal Variation in fractional cover: Explore, display, and assess (for 5 sites visited twice).

Latitudinal Pattern in Proportional Vegetation Cover

In this seection we will follow these steps:

- Call the `fractional_cover` function on the extracted point intercept data. This calculation may take a few minutes for all AusPlots, so for this example we will work with a random subset of 200 randomly drawn sites.
- Plot the Latitudinal Pattern in Proportional Vegetation Cover (here we use the 'Proportion of Bare Ground'). To do this, we first enrich the dataset with additional variables including: 'Plot' (identifier for each Site-Visit combination), 'bioregion.f', 'longitude', and 'latitude'.
- Fit a Quadratic Model to the data and examine its Fit, as there appears to be a humpbacked relationship in the previous plot (higher proportionof bare ground in the arid inland at mid-latitudes).

```
# First, we call the fractional_cover function on the extracted point intercept data.
# NOTE: Calculation may take a few minutes for all AusPlots, so for this example
# we will pull out a subset of 200 randomly drawn sites to work with.
# The sets site composition will differ each time the script is run,
# as they are random subsets.


# Compute Fractional Cover using function 'fractional_cover`
# ------------------------------------------------------------
AP.200Locs.FC =
fractional_cover(AP.data$veg.PI[AP.data$veg.PI$site_location_name %in%
                                      sample(AP.data$site.info$site_location_name, 200), ])
# To use the Full Data set substitute the command above by this one:
# fractional_cover(AP.data$veg.PI[AP.data$veg.PI$site_location_name %in%
#                                 AP.data$site.info$site_location_name, ])
#AP.200Locs.FC = na.omit(AP.200Loc.FC)
head(AP.200Locs.FC)
```

```
##                       site_unique  bare brown green  NA.
## NSABHC0002-53597 NSABHC0002-53597  0.00  0.00 30.10 69.9
## NSABHC0006-53601 NSABHC0006-53601 22.87 26.53 50.59  0.0
## NSABHC0016-57105 NSABHC0016-57105 49.70 38.81 11.29  0.2
## NSABHC0019-57078 NSABHC0019-57078 15.74 48.32 35.94  0.0
## NSAMDD0005-56969 NSAMDD0005-56969 19.90 48.91 31.19  0.0
## NSAMDD0008-56955 NSAMDD0008-56955 22.48 47.82 29.50  0.2
```

```
# Enrich with: Bioregion, Latitude, and Longitude
# ------------------------------------------------
AP.200Locs.FC  = merge(AP.200Locs.FC, AP.data$site.info, by="site_unique")[,c("site_unique",
"bare", "brown", "green", "NA.", "bioregion.f", "longitude", "latitude")]
AP.200Locs.FC = na.omit(AP.200Locs.FC)
head(AP.200Locs.FC)
```

```
##        site_unique  bare brown green  NA. bioregion.f longitude  latitude
## 1 NSABHC0002-53597  0.00  0.00 30.10 69.9         BHC  141.4330 -31.92703
## 2 NSABHC0006-53601 22.87 26.53 50.59  0.0         BHC  141.7823 -31.88421
## 3 NSABHC0016-57105 49.70 38.81 11.29  0.2         BHC  141.0614 -31.83403
## 4 NSABHC0019-57078 15.74 48.32 35.94  0.0         BHC  141.5496 -32.51485
## 5 NSAMDD0005-56969 19.90 48.91 31.19  0.0         MDD  143.2039 -33.65619
## 6 NSAMDD0008-56955 22.48 47.82 29.50  0.2         MDD  141.0720 -33.43096
```

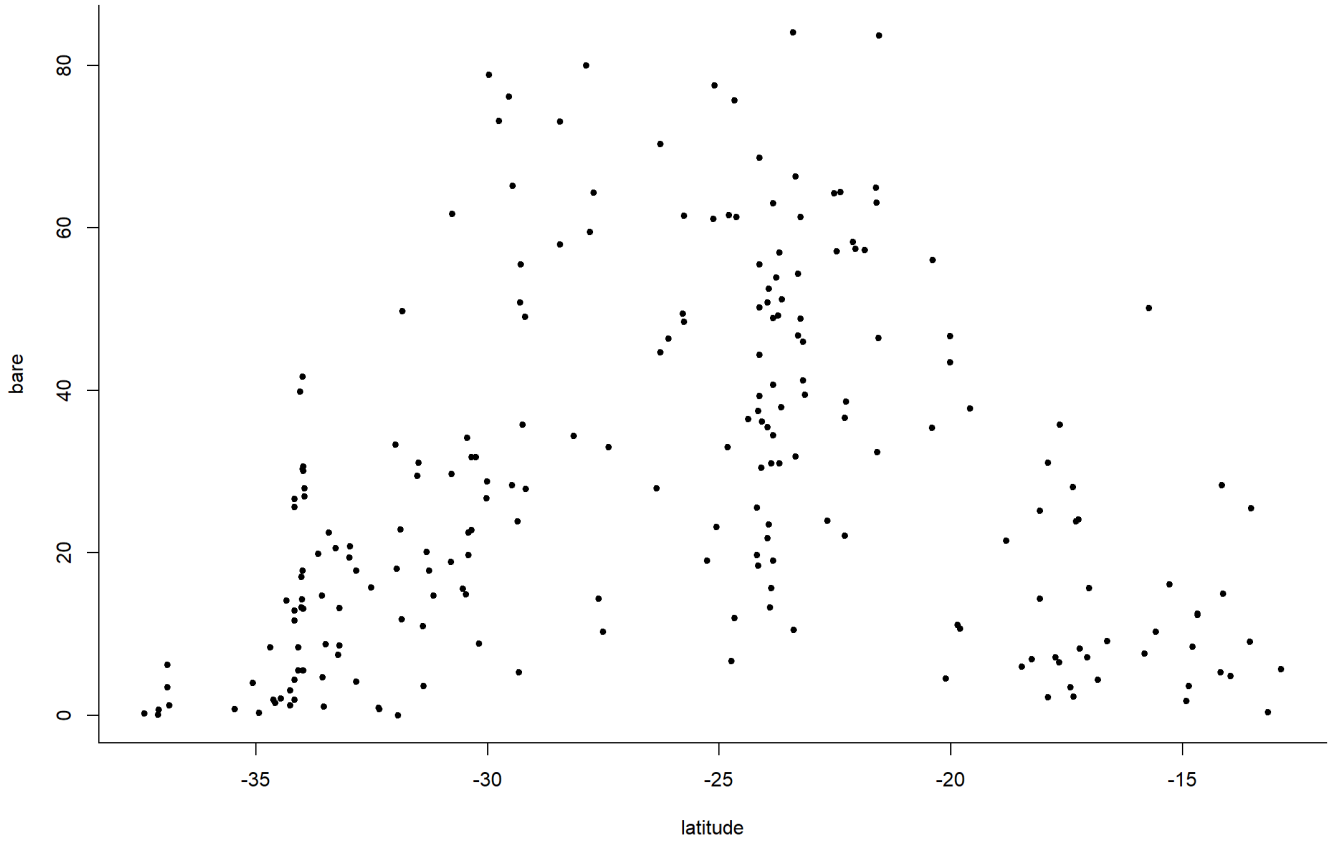
```
summary(AP.200Locs.FC)
```

```
##  site_unique             bare           brown           green      
##  Length:221         Min.   : 0.00   Min.   : 0.00   Min.   : 2.32  
##  Class :character   1st Qu.:10.30   1st Qu.:21.29   1st Qu.:21.58  
##  Mode  :character   Median :23.96   Median :32.38   Median :35.94  
##                     Mean   :28.51   Mean   :31.88   Mean   :39.03  
##                     3rd Qu.:44.70   3rd Qu.:40.99   3rd Qu.:54.85  
##                     Max.   :84.06   Max.   :65.15   Max.   :97.92  
##                                                                    
##       NA.           bioregion.f    longitude        latitude      
##  Min.   : 0.0000   SSD    : 26   Min.   :114.6   Min.   :-37.41  
##  1st Qu.: 0.0000   MDD    : 18   1st Qu.:133.3   1st Qu.:-31.95  
##  Median : 0.0000   RIV    : 15   Median :138.0   Median :-25.12  
##  Mean   : 0.5783   FLB    : 13   Mean   :135.3   Mean   :-26.27  
##  3rd Qu.: 0.0000   GFU    : 13   3rd Qu.:140.7   3rd Qu.:-22.29  
##  Max.   :69.9000   GUP    : 12   Max.   :150.6   Max.   :-12.87  
##                    (Other):124
```

```
names(AP.200Locs.FC)
```

```
## [1] "site_unique" "bare"        "brown"       "green"       "NA."
## [6] "bioregion.f" "longitude"   "latitude"
```

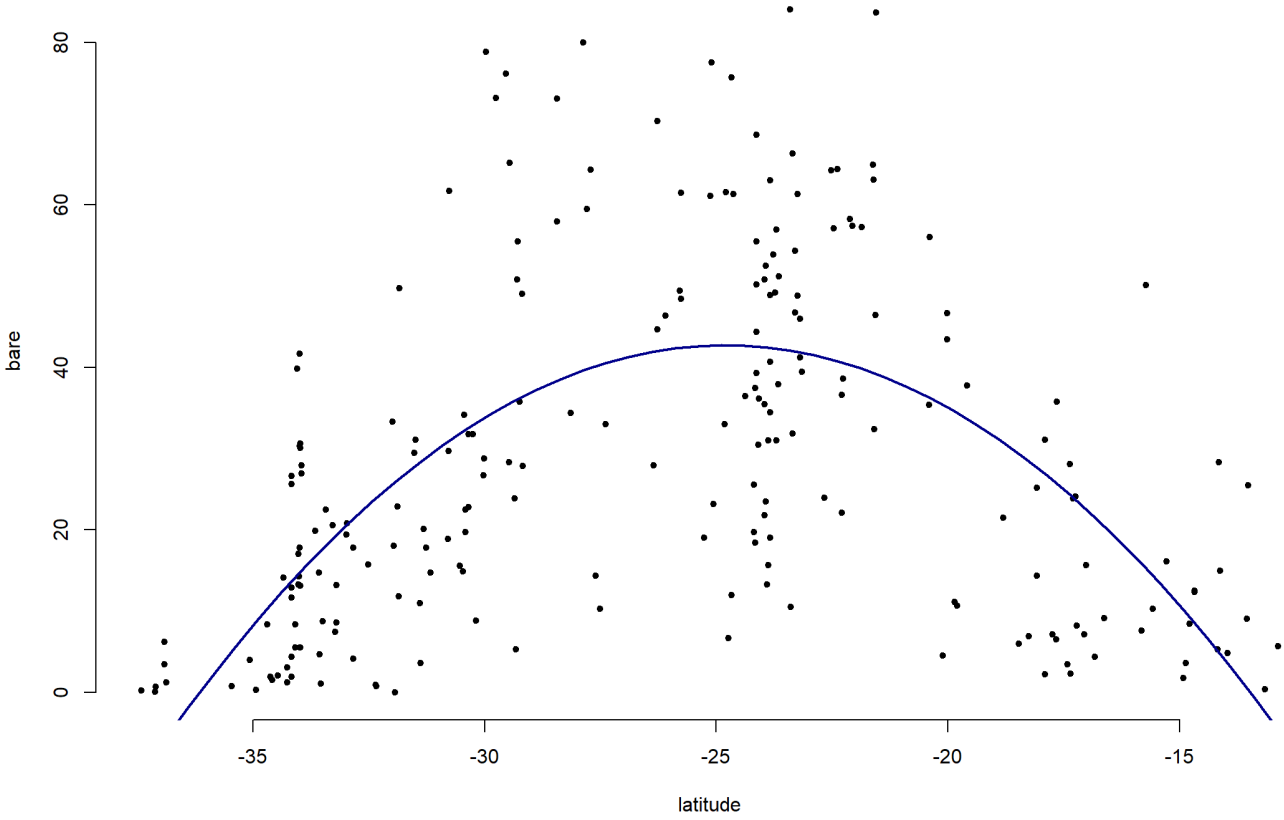
```
# Plot out the continental relationship between Fractional Cover
# ---------------------------------------------------------------
# Here we use the 'Proportion of Bare Ground' & Latitude

# Plot the relationship between Proportion of Bare Ground (with no kind of vegetation cover a
bove) and Latitude.
par(mfrow=c(1,1))
plot(bare ~ latitude, data=AP.200Locs.FC, pch=20, bty="l")
```




```
# Quadratic LM of Continental Relationship between Bare Ground Fractional Cover & Latitude
# ------------------------------------------------------------------------------------------

# Fit & Examine as Quadratic Linear Model the Continental Relationship between Bare Ground Fr
actional Cover & Latitude
AP.200Locs.FC.lm = lm(bare ~ latitude + I(latitude^2), data=AP.200Locs.FC)
summary(AP.200Locs.FC.lm)
```

```
##
## Call:
## lm(formula = bare ~ latitude + I(latitude^2), data = AP.200Locs.FC)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -36.104 -11.300  -1.221  10.179  44.917
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -161.83677   17.91572  -9.033   <2e-16 ***
## latitude       -16.48935    1.45418 -11.339   <2e-16 ***
## I(latitude^2)   -0.33228    0.02826 -11.757   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.81 on 218 degrees of freedom
## Multiple R-squared:  0.4004, Adjusted R-squared:  0.3949
## F-statistic: 72.79 on 2 and 218 DF,  p-value: < 2.2e-16
```

```
# Predict values from Model Fit
pred.df = data.frame(latitude=seq(from=min(AP.200Locs.FC$latitude), to=max(AP.200Locs.FC$lati
tude), length.out=50))
pred.df$pred = predict(AP.200Locs.FC.lm, pred.df)

# Plot Predicted Values from Model Fit on Graph with Continental Relationship between Bare Gr
ound Fractional Cover & Latitude
plot(bare ~ latitude, data=AP.200Locs.FC, pch=20, bty="n")
points(pred.df$latitude, pred.df$pred, type="l", lwd=2, col="darkblue")
```



Temporal Variation in Fractional Cover: Explore, display, and assess (for 5 sites visited twice)

In the second section on Fractional Cover, we first Identify Sites that have been sampled more than once over time (in the 5 most sampled bioregions). Then we visually compare the Temporal Variation in Fractional Cover in these sites using Piecharts.

```
# Find Sites Sampled > 1 time
# --------------------------
# Extract Sites Names
AP.200Locs.FC.locs = sub("\\-.*", "", AP.200Locs.FC$site_unique)
length(AP.200Locs.FC.locs)
```

```
## [1] 221
```

```
# Calculate the Sample Frequency of each Site
AP.200Locs.FC.locs.cnt = count(AP.200Locs.FC.locs)
dim(AP.200Locs.FC.locs.cnt)
```

```
## [1] 197   2
```

```
# Find Sites with > 1 Samples (in veg.IP)
AP.200Locs.FC.Resampled.locs.cnt = AP.200Locs.FC.locs.cnt[AP.200Locs.FC.locs.cnt$freq > 1,]
dim(AP.200Locs.FC.Resampled.locs.cnt)
```

```
## [1] 24  2
```

```
AP.200Locs.FC.Resampled.locs.cnt = AP.200Locs.FC.Resampled.locs.cnt$x
length(AP.200Locs.FC.Resampled.locs.cnt)
```

```
## [1] 24
```

```
# Subset the Resampled Sites (i.e. with 'freq' > 1)
# ------------------------------------------------
# Extract AP.200Locs.FC subset for Sites with > 1 Samples (in veg.IP)
AP.200Locs.FC.Resampled.Locs = AP.200Locs.FC[(AP.200Locs.FC.locs %in% AP.200Locs.FC.Resample
d.locs.cnt),]
#AP.200Locs.FC.Resampled.Locs
dim(AP.200Locs.FC.Resampled.Locs) # 82 (= 41 * 2)
```

```
## [1] 48  8
```

```
# Add Year (Started) Sampling of Site-Visit Pair
# ----------------------------------------------
# Need to specify 'AP.BioregTop5.l$site.info[,c("site_unique","visit_start_date")]' to avoid
 duplicate columns
AP.200Locs.FC.Resampled.Locs  = merge(AP.200Locs.FC.Resampled.Locs, AP.BioregTop5.l$site.info
[,c("site_unique","visit_start_date")],
                                                    by="site_unique")[,c(names(AP.200Loc
s.FC.Resampled.Locs),                                                    "visit_start_date")]
names(AP.200Locs.FC.Resampled.Locs)
```

```
## [1] "site_unique"      "bare"             "brown"
## [4] "green"            "NA."              "bioregion.f"
## [7] "longitude"        "latitude"         "visit_start_date"
```

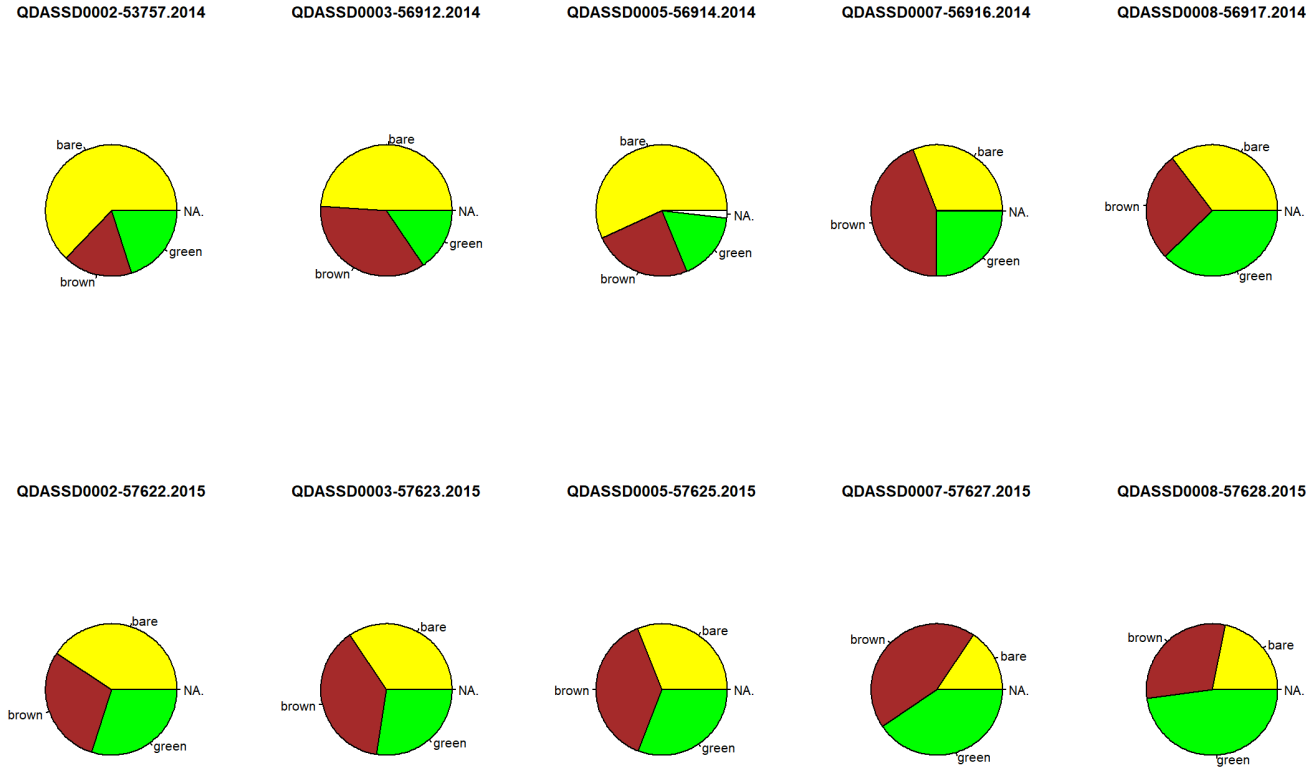
```
#AP.200Locs.FC.Resampled.Locs$visit_start_date
#substr(AP.200Locs.FC.Resampled.Locs$visit_start_date,1,4)
AP.200Locs.FC.Resampled.Locs$site_unique.Yr = paste( AP.200Locs.FC.Resampled.Locs$site_uniqu
e,
                                             substr(AP.200Locs.FC.Resampled.Locs$visit_start
_date,1,4),
                                             sep="." )
head(AP.200Locs.FC.Resampled.Locs$site_unique.Yr)
```

```
## [1] "QDASSD0002-53757.2014" "QDASSD0002-57622.2015" "QDASSD0003-56912.2014"
## [4] "QDASSD0003-57623.2015" "QDASSD0005-56914.2014" "QDASSD0005-57625.2015"
```

```
# Plot Pies for the first 5 Resampled Sites -out of 41- (i.e. 10 Site-Visit pairs)
# ------------------------------------------------------------------------------
# Order dataframe to Plot Site-Visit pairs in the appropriate order
AP.200Locs.FC.Resampled.Locs = AP.200Locs.FC.Resampled.Locs[order(AP.200Locs.FC.Resampled.Loc
s$site_unique),]
head(AP.200Locs.FC.Resampled.Locs)
```

```
##        site_unique  bare brown green  NA. bioregion.f longitude  latitude
## 1 QDASSD0002-53757 62.97 16.93 20.10 0.00         SSD  138.3897 -23.82772
## 2 QDASSD0002-57622 40.69 29.50 29.80 0.00         SSD  138.3897 -23.82772
## 3 QDASSD0003-56912 48.91 35.45 15.64 0.00         SSD  138.4074 -23.83157
## 4 QDASSD0003-57623 34.42 38.08 27.50 0.00         SSD  138.4074 -23.83157
## 5 QDASSD0005-56914 56.93 24.36 16.83 1.88         SSD  138.4410 -23.69444
## 6 QDASSD0005-57625 31.02 38.06 30.91 0.00         SSD  138.4410 -23.69444
##      visit_start_date        site_unique.Yr
## 1 2014-05-01T00:00:00 QDASSD0002-53757.2014
## 2 2015-04-16T00:00:00 QDASSD0002-57622.2015
## 3 2014-05-01T00:00:00 QDASSD0003-56912.2014
## 4 2015-04-16T00:00:00 QDASSD0003-57623.2015
## 5 2014-05-02T00:00:00 QDASSD0005-56914.2014
## 6 2015-04-26T00:00:00 QDASSD0005-57625.2015
```

```
# Plot the Site-Visit pairs
par(mfcol=c(2,5))
for (site.visit.cnt in 1:10) {

    pie( x=as.numeric(AP.200Locs.FC.Resampled.Locs[site.visit.cnt,2:5]),
         col=c("yellow", "brown", "green", "white"),
         labels=names(AP.200Locs.FC.Resampled.Locs[2:5]),
         main=as.character(AP.200Locs.FC.Resampled.Locs[site.visit.cnt,"site_unique.Yr"]) )

}  # for site.visit.cnt in 1:20 {
```



GROWTH FORM: `growth_form_table` function (for 5 most sampled bioregions)

The `growth_form_table` function in the `ausplotR` package can be used to generate occurrence matrices for NVIS plant growth forms in plots. The input for this function is a data frame of raw point intercept AusPlots data generated using the `get_ausplots` function. Three metrics can be selected to score species growth form:

- *Presence/Absence* (argument `m_kind = PA`).
- *Percent Cover*: Based on total frequency of hits (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*: (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 sometimes 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.

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

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

In this section we will:

- Generate a Plant Growth Forms Percent Cover against Sites Matrix using the `growth_form_table` function.
- Enrich this Matrix with additional information (plot -site-visit-, bioregion, longitude, and latitude).
- Compute Summary Statics for each of the Growth Forms in the 5 most sampled Bioregions (slightly different to those produce by the `summary` function in the `base` package.

- Cluster (Hierachical Clustering) the Sites-Visits by Plant Growth Forms Percent Cover, colouring the resulting tree branches by bioregion.

CLUSTERING RESULTS:

- The first Site-Visit (NTAGFU0007-53654) is very different to the rest
- The dendrogram shows clusters formed by single Bioregions at low level; however, at higher-level clusters are composed by Sites-Visits from different Bioregions.

```
# Generate the Growth Form by Site-Visit Matrix
# =============================================
AP.BRTop5.GrowthFormBYSites = growth_form_table(AP.BioregTop5.l$veg.PI,
m_kind="percent_cover", cover_type="PFC")  # % Cover
dim(AP.BRTop5.GrowthFormBYSites) # No of rows and cols in Matrix: 574 Sites x 19 Growth Forms
```

```
## [1] 210  15
```

```
head(AP.BRTop5.GrowthFormBYSites)
```

```
##                   Chenopod  Epiphyte Fern       Forb    Fungus
## NSAMDD0001-56965 19.537815 0.0000000    0 83.1932773 0.4201681
## NSAMDD0002-56952  3.024911 0.0000000    0  0.1779359 0.0000000
## NSAMDD0003-56968 24.635036 0.0000000    0  9.3065693 0.0000000
## NSAMDD0004-56953 45.194805 0.0000000    0 31.9480519 0.0000000
## NSAMDD0005-56969 12.923077 0.0000000    0 12.0000000 0.0000000
## NSAMDD0006-56954 79.945799 0.2710027    0  3.2520325 0.0000000
##                  Hummock.grass        NC Rush Sedge      Shrub
## NSAMDD0001-56965       0.00000 2.7310924    0     0  0.0000000
## NSAMDD0002-56952      31.13879 0.0000000    0     0  1.6014235
## NSAMDD0003-56968       0.00000 0.0000000    0     0 82.8467153
## NSAMDD0004-56953       0.00000 0.0000000    0     0  5.1948052
## NSAMDD0005-56969       0.00000 0.9230769    0     0  4.0000000
## NSAMDD0006-56954       0.00000 0.0000000    0     0  0.8130081
##                  Shrub.Mallee Tree.Mallee Tree.Palm Tussock.grass Vine
## NSAMDD0001-56965    0.0000000   0.0000000  0.000000     1.8907563    0
## NSAMDD0002-56952    0.5338078  76.8683274  0.000000     0.3558719    0
## NSAMDD0003-56968    0.0000000   0.3649635  1.094891     0.0000000    0
## NSAMDD0004-56953    0.0000000   0.0000000 28.831169     1.0389610    0
## NSAMDD0005-56969    0.0000000  76.6153846  0.000000     0.3076923    0
## NSAMDD0006-56954    0.0000000   0.0000000 32.249322     0.5420054    0
```

```
# Enrich DF
# =========

# Create a 'site_unique' variable in Growth Form by Site-VisitTable to relate both datasets
# ------------------------------------------------------------------------------------------
AP.BRTop5.GrowthFormBYSites$site_unique = rownames(AP.BRTop5.GrowthFormBYSites)

# Add: Bioregion, Longitude, Latitude
# -----------------------------------
# Both DF have different number of rows (again!)
dim(AP.BRTop5.GrowthFormBYSites)
```

```
## [1] 210  16
```

```
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
AP.BRTop5.GrowthFormBYSites  = merge(AP.BRTop5.GrowthFormBYSites, AP.BioregTop5.l$site.info,
 by="site_unique")[,c(names(AP.BRTop5.GrowthFormBYSites),

"bioregion.f", "longitude", "latitude")]
AP.BRTop5.GrowthFormBYSites = na.omit(AP.BRTop5.GrowthFormBYSites)
#head(AP.BRTop5.GrowthFormBYSites)
summary(AP.BRTop5.GrowthFormBYSites)
```

```
##     Chenopod          Epiphyte            Fern              Forb
##  Min.   :  0.000   Min.   :0.00000   Min.   :0.00000   Min.   : 0.000
##  1st Qu.:  0.000   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.: 1.537
##  Median :  1.326   Median :0.00000   Median :0.00000   Median : 6.634
##  Mean   : 13.980   Mean   :0.05155   Mean   :0.08329   Mean   :14.526
##  3rd Qu.: 20.625   3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:19.292
##  Max.   :100.000   Max.   :2.97483   Max.   :3.22581   Max.   :94.268
##      Fungus         Hummock.grass          NC                Rush
##  Min.   :0.000000   Min.   :  0.00   Min.   :0.00000   Min.   :0.000000
##  1st Qu.:0.000000   1st Qu.:  0.00   1st Qu.:0.00000   1st Qu.:0.000000
##  Median :0.000000   Median :  0.00   Median :0.00000   Median :0.000000
##  Mean   :0.002001   Mean   : 16.17   Mean   :0.06386   Mean   :0.004657
##  3rd Qu.:0.000000   3rd Qu.: 21.75   3rd Qu.:0.00000   3rd Qu.:0.000000
##  Max.   :0.420168   Max.   :183.86   Max.   :2.80374   Max.   :0.764331
##      Sedge              Shrub         Shrub.Mallee      Tree.Mallee
##  Min.   : 0.0000   Min.   : 0.000   Min.   : 0.0000   Min.   : 0.000
##  1st Qu.: 0.0000   1st Qu.: 2.507   1st Qu.: 0.0000   1st Qu.: 0.000
##  Median : 0.0000   Median : 8.856   Median : 0.0000   Median : 0.000
##  Mean   : 0.7123   Mean   :19.112   Mean   : 0.6793   Mean   : 6.773
##  3rd Qu.: 0.0000   3rd Qu.:27.945   3rd Qu.: 0.0000   3rd Qu.: 0.000
##  Max.   :21.6561   Max.   :91.042   Max.   :37.7863   Max.   :91.979
##    Tree.Palm       Tussock.grass         Vine         site_unique
##  Min.   : 0.0000   Min.   : 0.000   Min.   : 0.0000   Length:210
##  1st Qu.: 0.0000   1st Qu.: 2.106   1st Qu.: 0.0000   Class :character
##  Median : 0.4028   Median :16.233   Median : 0.0000   Mode  :character
##  Mean   :12.7666   Mean   :27.149   Mean   : 0.3825
##  3rd Qu.:15.3223   3rd Qu.:45.799   3rd Qu.: 0.0000
##  Max.   :99.1747   Max.   :99.051   Max.   :26.1456
##  bioregion.f   longitude        latitude
##  GFU:41      Min.   :117.0   Min.   :-35.00
##  MDD:50      1st Qu.:134.9   1st Qu.:-29.78
##  PIL:35      Median :136.8   Median :-25.12
##  SSD:46      Mean   :134.9   Mean   :-25.38
##  STP:38      3rd Qu.:139.2   3rd Qu.:-21.88
##              Max.   :145.8   Max.   :-14.05
```

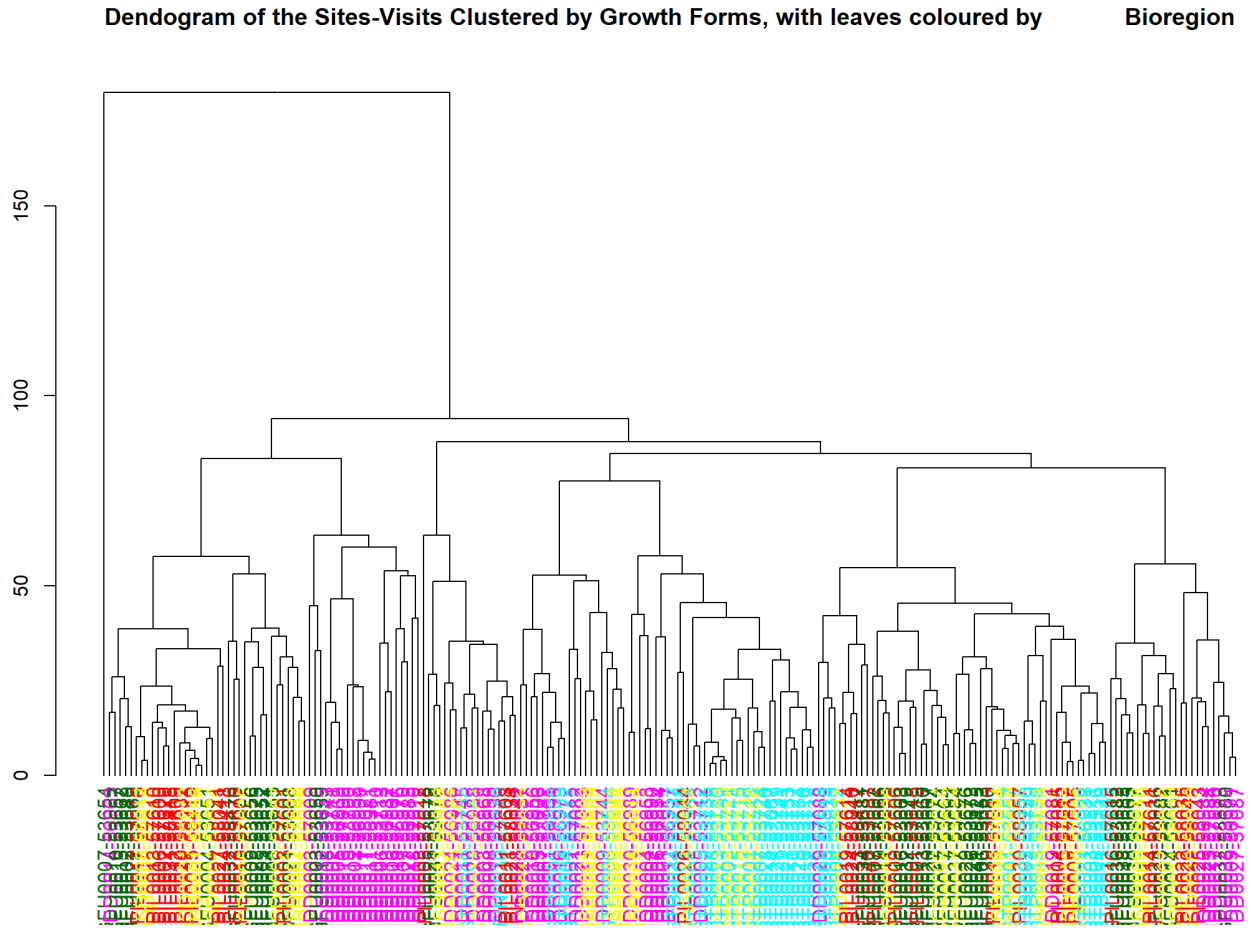
```
names(AP.BRTop5.GrowthFormBYSites)
```

```
##  [1] "Chenopod"      "Epiphyte"      "Fern"          "Forb"
##  [5] "Fungus"        "Hummock.grass" "NC"            "Rush"
##  [9] "Sedge"         "Shrub"         "Shrub.Mallee"  "Tree.Mallee"
## [13] "Tree.Palm"     "Tussock.grass" "Vine"          "site_unique"
## [17] "bioregion.f"   "longitude"     "latitude"
```

```
# Summary Statistics for Each Growth Form
# =======================================
AP.BRTop5.GFBYSites.DescStats = data.frame(
  Min = apply(AP.BRTop5.GrowthFormBYSites[,1:(dim(AP.BRTop5.GrowthFormBYSites)[2]-4)], 2,
min), # Minimum
  Med = apply(AP.BRTop5.GrowthFormBYSites[,1:(dim(AP.BRTop5.GrowthFormBYSites)[2]-4)], 2,
median), # Median
  Max = apply(AP.BRTop5.GrowthFormBYSites[,1:(dim(AP.BRTop5.GrowthFormBYSites)[2]-4)], 2,
max), # Maximum
  Mean = apply(AP.BRTop5.GrowthFormBYSites[,1:(dim(AP.BRTop5.GrowthFormBYSites)[2]-4)], 2,
mean), # Mean
  SD = apply(AP.BRTop5.GrowthFormBYSites[,1:(dim(AP.BRTop5.GrowthFormBYSites)[2]-4)], 2,
sd) # Standard Deviation
  )
AP.BRTop5.GFBYSites.DescStats = round(AP.BRTop5.GFBYSites.DescStats, 2)
AP.BRTop5.GFBYSites.DescStats
```

```
##               Min   Med    Max  Mean    SD
## Chenopod        0  1.33 100.00 13.98 22.31
## Epiphyte        0  0.00   2.97  0.05  0.28
## Fern            0  0.00   3.23  0.08  0.39
## Forb            0  6.63  94.27 14.53 18.91
## Fungus          0  0.00   0.42  0.00  0.03
## Hummock.grass   0  0.00 183.86 16.17 29.04
## NC              0  0.00   2.80  0.06  0.33
## Rush            0  0.00   0.76  0.00  0.05
## Sedge           0  0.00  21.66  0.71  2.82
## Shrub           0  8.86  91.04 19.11 22.38
## Shrub.Mallee    0  0.00  37.79  0.68  4.03
## Tree.Mallee     0  0.00  91.98  6.77 17.58
## Tree.Palm       0  0.40  99.17 12.77 22.55
## Tussock.grass   0 16.23  99.05 27.15 27.82
## Vine            0  0.00  26.15  0.38  2.05
```

```
# Create and Plot a Dendogram of the Sites-Visits Clustered by Growth Forms
# ========================================================================

# Add rownames to be used as Leaves Names
rownames(AP.BRTop5.GrowthFormBYSites) = AP.BRTop5.GrowthFormBYSites$site_unique

# Create Dendogram
AP.BRTop5.GFBYSites.dend = as.dendrogram(hclust(dist(AP.BRTop5.GrowthFormBYSites[,1: (dim(AP.
BRTop5.GrowthFormBYSites)[2]-4)]), "average"))

# Color the Leaves by Bioregion
# NOTE: The most sampled bioregions might change as new data is added. If so, bioregions code
s bellow should be revised.
# Here the codes correspond to: MDD (Murry Darling Depression), SSD (Simpson
# Strzelecki Dunefields), GFU (Gulf Fall and Uplands), STP (Stony Plains),
# PIL (Pilbara)
AP.BRTop5.GrowthFormBYSites$bioregion.col.f = AP.BRTop5.GrowthFormBYSites$bioregion.f
levels(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)[levels(AP.BRTop5.GrowthFormBYSites$bioreg
ion.col.f) == "GFU"] = "darkgreen"
levels(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)[levels(AP.BRTop5.GrowthFormBYSites$bioreg
ion.col.f) == "MDD"] = "magenta"
levels(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)[levels(AP.BRTop5.GrowthFormBYSites$bioreg
ion.col.f) == "PIL"] = "red"
levels(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)[levels(AP.BRTop5.GrowthFormBYSites$bioreg
ion.col.f) == "SSD"] = "yellow"
levels(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)[levels(AP.BRTop5.GrowthFormBYSites$bioreg
ion.col.f) == "STP"] = "cyan"
dend.colors = as.character(AP.BRTop5.GrowthFormBYSites$bioregion.col.f)
#dend.colors
dend.colors = dend.colors[order.dendrogram(AP.BRTop5.GFBYSites.dend)]
#dend.colors
labels_colors(AP.BRTop5.GFBYSites.dend) = dend.colors
# Plot Dendrogram
par(mfrow=c(1,1))
plot(AP.BRTop5.GFBYSites.dend,
     main="Dendogram of the Sites-Visits Clustered by Growth Forms, with leaves coloured by
Bioregion")
```



TOTAL VEGETATION COVER BY GROWTH FORM AND/OR HEIGHT: `single_cover_value` function (for 5 most sampled bioregions).

Similar to the `growth_form_table` function, the `single_cover_value` function can calculate Vegetation Cover Values per Site from Raw Vegetation Point Intercept data from AusPlots. However, the `single_cover_value` can perform these computations for:

1. Vegetation of *particular growth form types* (i.e. for individual growth form types or any combination of growth form types).
2. Vegetation *higher that a specified height threshold*
3. Vegetation with any combination of *growth form types* and *minimum height*

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

- *Raw Vegetation Point Intercept data from AusPlots* (argument `veg.PI`): A `veg.PI` data frame generated by the `get_ausplots` function (see above).
- *Method used to Calculate Cover* (argument `in_canopy_sky`): 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.
- *Whether to Calculate Cover for a Subset by Growth Form Type* (argument `by.growth_form`): 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`. If set to `FALSE` cover calculations are conducted only for the vegetation subsetted by a Minimum Height.
- *Growth Form Types used to Subset Data used for the Cover Calculations* (argument `my.growth_forms`): 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 subsetting is applied.

- *Minimum Height Threshold used to Subset Data used for the Cover Calculations* (argument `min.height`): A numeric value indicating the minimum height (in metres) of the vegetation to 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 zero to ignore height and include any plant hit. If set to a negative number, it will return nonsensical output.

When `by.growth_form = FALSE` and `min.height = 0`, the output is nearly the same as the green cover fraction returned from `fractional_cover`. 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 (e.g. when dead trees overhang green understorey). For such general cover purposes, using `fractional_cover` is recommended. `single_cover_value` is best suited to cover subset by height and growth form.

Next, several examples of how to compute, manipulate, and visualise 'Single' Vegetation Cover Fraction (VCF) data are presented. The examples cover different scenarios for subsetting the input vegetation point intercept data frame prior to the calculation of the corresponding VCF. These include:

- Subsetting only by Height
- Subsetting only by Taxonomoy
- Subsetting by Height and Taxonomy

Subsetting by Height only

```
# Subsetting by Height only
# *************************

# Compute Single Cover Values Tables
# ==================================
# Any green vegeation (i.e. >= 0m in height)
veg.cover.gt0 = single_cover_value(AP.BioregTop5.l$veg.PI, by.growth_form=FALSE, min.height=0
)
# Any green vegeation >= 2m in height
veg.cover.gt2 = single_cover_value(AP.BioregTop5.l$veg.PI, by.growth_form=FALSE, min.height=2
)


# Combine all Tables into a Sigle Data Frame
# ==========================================
# Create a data frame containing all the Vegetation Cover Fractions
AP.BioregTop5.VCF.df = data.frame(site_unique=veg.cover.gt0$site_unique, VCF.gt0=veg.cover.gt
0$percentCover, VCF.gt2=veg.cover.gt2$percentCover)
head(AP.BioregTop5.VCF.df)
```

```
##        site_unique VCF.gt0 VCF.gt2
## 1 NSAMDD0001-56965   45.74    0.00
## 2 NSAMDD0002-56952   55.45   39.21
## 3 NSAMDD0003-56968   47.52    4.65
## 4 NSAMDD0004-56953   35.05   10.99
## 5 NSAMDD0005-56969   31.29   23.76
## 6 NSAMDD0006-56954   34.95   11.29
```

```
summary(AP.BioregTop5.VCF.df)
```

```
##            site_unique     VCF.gt0         VCF.gt2
##  NSAMDD0001-56965:  1   Min.   : 0.20   Min.   : 0.00
##  NSAMDD0002-56952:  1   1st Qu.:20.02   1st Qu.: 0.10
##  NSAMDD0003-56968:  1   Median :32.03   Median : 4.80
##  NSAMDD0004-56953:  1   Mean   :34.59   Mean   :10.61
##  NSAMDD0005-56969:  1   3rd Qu.:47.76   3rd Qu.:16.19
##  NSAMDD0006-56954:  1   Max.   :79.90   Max.   :67.33
##  (Other)         :204
```

```
# Enrich DF
# =========

# Compute Vegetation Cover Fractions for Height Ranges
# ----------------------------------------------------
AP.BioregTop5.VCF.df$VCF.0to2 = AP.BioregTop5.VCF.df$VCF.gt0 - AP.BioregTop5.VCF.df$VCF.gt2
head(AP.BioregTop5.VCF.df)
```

```
##        site_unique VCF.gt0 VCF.gt2 VCF.0to2
## 1 NSAMDD0001-56965   45.74    0.00    45.74
## 2 NSAMDD0002-56952   55.45   39.21    16.24
## 3 NSAMDD0003-56968   47.52    4.65    42.87
## 4 NSAMDD0004-56953   35.05   10.99    24.06
## 5 NSAMDD0005-56969   31.29   23.76     7.53
## 6 NSAMDD0006-56954   34.95   11.29    23.66
```

```
summary(AP.BioregTop5.VCF.df)
```

```
##            site_unique     VCF.gt0         VCF.gt2         VCF.0to2
##  NSAMDD0001-56965:  1   Min.   : 0.20   Min.   : 0.00   Min.   : 0.20
##  NSAMDD0002-56952:  1   1st Qu.:20.02   1st Qu.: 0.10   1st Qu.:12.28
##  NSAMDD0003-56968:  1   Median :32.03   Median : 4.80   Median :20.79
##  NSAMDD0004-56953:  1   Mean   :34.59   Mean   :10.61   Mean   :23.98
##  NSAMDD0005-56969:  1   3rd Qu.:47.76   3rd Qu.:16.19   3rd Qu.:33.34
##  NSAMDD0006-56954:  1   Max.   :79.90   Max.   :67.33   Max.   :68.02
##  (Other)         :204
```

```
# Add: Bioregion, Longitude, Latitude
# -----------------------------------

# Both DF have different number of rows
dim(AP.BioregTop5.VCF.df)
```

```
## [1] 210   4
```

```
dim(AP.BioregTop5.1$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
AP.BioregTop5.VCF.df  = merge(AP.BioregTop5.VCF.df, AP.BioregTop5.l$site.info, by="site_uniqu
e")[,c(names(AP.BioregTop5.VCF.df), "bioregion.f", "longitude", "latitude")]
AP.BioregTop5.VCF.df = na.omit(AP.BioregTop5.VCF.df)
head(AP.BioregTop5.VCF.df)
```

```
##        site_unique VCF.gt0 VCF.gt2 VCF.0to2 bioregion.f longitude
## 1 NSAMDD0001-56965   45.74    0.00    45.74         MDD  142.5602
## 2 NSAMDD0002-56952   55.45   39.21    16.24         MDD  142.6026
## 3 NSAMDD0003-56968   47.52    4.65    42.87         MDD  142.6041
## 4 NSAMDD0004-56953   35.05   10.99    24.06         MDD  142.5594
## 5 NSAMDD0005-56969   31.29   23.76     7.53         MDD  143.2039
## 6 NSAMDD0006-56954   34.95   11.29    23.66         MDD  143.1665
##    latitude
## 1 -34.18392
## 2 -34.20482
## 3 -34.20754
## 4 -34.16537
## 5 -33.65619
## 6 -33.66432
```

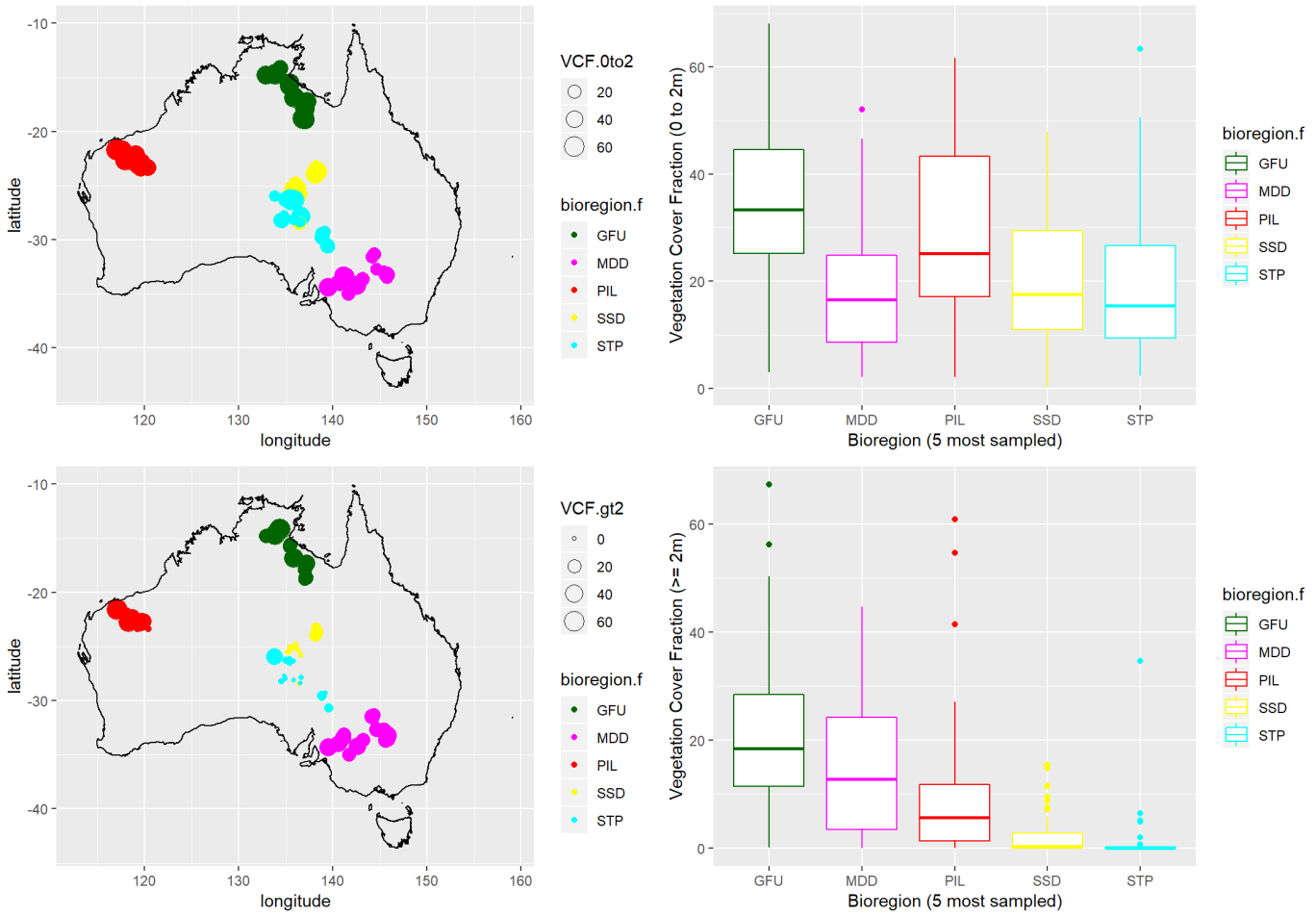
```
summary(AP.BioregTop5.VCF.df)
```

```
##            site_unique     VCF.gt0         VCF.gt2         VCF.0to2
##  NSAMDD0001-56965:  1   Min.   : 0.20   Min.   : 0.00   Min.   : 0.20
##  NSAMDD0002-56952:  1   1st Qu.:20.02   1st Qu.: 0.10   1st Qu.:12.28
##  NSAMDD0003-56968:  1   Median :32.03   Median : 4.80   Median :20.79
##  NSAMDD0004-56953:  1   Mean   :34.59   Mean   :10.61   Mean   :23.98
##  NSAMDD0005-56969:  1   3rd Qu.:47.76   3rd Qu.:16.19   3rd Qu.:33.34
##  NSAMDD0006-56954:  1   Max.   :79.90   Max.   :67.33   Max.   :68.02
##  (Other)         :204
##  bioregion.f   longitude        latitude
##  GFU:41      Min.   :117.0   Min.   :-35.00
##  MDD:50      1st Qu.:134.9   1st Qu.:-29.78
##  PIL:35      Median :136.8   Median :-25.12
##  SSD:46      Mean   :134.9   Mean   :-25.38
##  STP:38      3rd Qu.:139.2   3rd Qu.:-21.88
##              Max.   :145.8   Max.   :-14.05
##
```

```
names(AP.BioregTop5.VCF.df)
```

```
## [1] "site_unique" "VCF.gt0"     "VCF.gt2"     "VCF.0to2"    "bioregion.f"
## [6] "longitude"   "latitude"
```

```
# Graphical Visualisation
# ======================

# VCF 0 to 2m: Map with circle size = the Vegetation Cover Fraction for any green veg.
# ------------------------------------------------------------------------------------
# (i.e. >= 0m in height)
AP.BioregTop5.VCF.df.p1 =
ggplot(data=AP.BioregTop5.VCF.df, aes(x=longitude, y=latitude, colour=bioregion.f, fill=biore
gion.f), alpha =0.5) +
geom_point(aes(size=VCF.0to2), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# VCF 0 to 2m: Boxplot
# --------------------
AP.BioregTop5.VCF.df.p2 =
ggplot(AP.BioregTop5.VCF.df, aes(x=bioregion.f, y=VCF.0to2, color=bioregion.f)) +
geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(x="Bioregion (5 most sampled)", y = "Vegetation Cover Fraction (0 to 2m)") +
theme(plot.title = element_text(hjust = 0.5))

# VCF >= 2m: Map with circle size = the Vegetation Cover Fraction for any green veg.
# ----------------------------------------------------------------------------------
# (i.e. >= 0m in height)
AP.BioregTop5.VCF.df.p3 =
ggplot(data=AP.BioregTop5.VCF.df, aes(x=longitude, y=latitude, colour=bioregion.f, fill=biore
gion.f), alpha =0.5) +
geom_point(aes(size=VCF.gt2), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# VCF  >= 2m: Boxplot
# -------------------
AP.BioregTop5.VCF.df.p4 =
ggplot(AP.BioregTop5.VCF.df, aes(x=bioregion.f, y=VCF.gt2, color=bioregion.f)) +
geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(x="Bioregion (5 most sampled)", y = "Vegetation Cover Fraction (>= 2m)") +
theme(plot.title = element_text(hjust = 0.5))

# Plot both graphs
# ----------------
grid.arrange(AP.BioregTop5.VCF.df.p1, AP.BioregTop5.VCF.df.p2,
             AP.BioregTop5.VCF.df.p3, AP.BioregTop5.VCF.df.p4, nrow=2)
```




```
#grid.arrange(AP.BioregTop5.VCF.df.p1, AP.BioregTop5.VCF.df.p2,
#              AP.BioregTop5.VCF.df.p3, AP.BioregTop5.VCF.df.p4, ncol=2)
```

Subsetting by Taxonomy only

```
# Subsetting y Taxonomy only
# **************************

# Compute Single Cover Values Tables
# ==================================
# Trees (by default my.growth_forms=c("Tree/Palm", "Tree Mallee"))
veg.cover.trees = single_cover_value(AP.BioregTop5.l$veg.PI, min.height=0)
# Grasses (my.growth_forms=c("Hummock.grass", "Tussock.grass"))
veg.cover.grass = single_cover_value(AP.BioregTop5.l$veg.PI, by.growth_form=TRUE, my.growth_f
orms=c("Hummock grass", "Tussock grass"), min.height=0)


# Combine all Tables into a Sigle Data Frame
# ==========================================
# Create a data frame containing all the Vegetation Cover Fractions
AP.BioregTop5.VCF.df = data.frame(site_unique=veg.cover.trees$site_unique, VCF.trees=veg.cove
r.trees$percentCover, VCF.grass=veg.cover.grass$percentCover)
head(AP.BioregTop5.VCF.df)
```

```
##        site_unique VCF.trees VCF.grass
## 1 NSAMDD0001-56965      0.00      0.89
## 2 NSAMDD0002-56952     42.57     17.33
## 3 NSAMDD0003-56968      0.20      0.00
## 4 NSAMDD0004-56953     10.40      0.00
## 5 NSAMDD0005-56969     24.65      0.10
## 6 NSAMDD0006-56954     11.68      0.00
```

```
summary(AP.BioregTop5.VCF.df)
```

```
##            site_unique    VCF.trees        VCF.grass
##  NSAMDD0001-56965:  1   Min.   : 0.000   Min.   : 0.000
##  NSAMDD0002-56952:  1   1st Qu.: 0.000   1st Qu.: 1.415
##  NSAMDD0003-56968:  1   Median : 1.190   Median : 9.700
##  NSAMDD0004-56953:  1   Mean   : 8.066   Mean   :16.420
##  NSAMDD0005-56969:  1   3rd Qu.:12.480   3rd Qu.:28.585
##  NSAMDD0006-56954:  1   Max.   :67.030   Max.   :67.430
##  (Other)         :204
```

```
# Enrich DF
# =========

# Add: Bioregion, Longitude, Latitude
# -----------------------------------

# Both DF have different number of rows
dim(AP.BioregTop5.VCF.df)
```

```
## [1] 210   3
```

```
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
AP.BioregTop5.VCF.df  = merge(AP.BioregTop5.VCF.df, AP.BioregTop5.l$site.info, by="site_uniqu
e")[,c(names(AP.BioregTop5.VCF.df), "bioregion.f", "longitude", "latitude")]
AP.BioregTop5.VCF.df = na.omit(AP.BioregTop5.VCF.df)
head(AP.BioregTop5.VCF.df)
```

```
##        site_unique VCF.trees VCF.grass bioregion.f longitude  latitude
## 1 NSAMDD0001-56965      0.00      0.89         MDD  142.5602 -34.18392
## 2 NSAMDD0002-56952     42.57     17.33         MDD  142.6026 -34.20482
## 3 NSAMDD0003-56968      0.20      0.00         MDD  142.6041 -34.20754
## 4 NSAMDD0004-56953     10.40      0.00         MDD  142.5594 -34.16537
## 5 NSAMDD0005-56969     24.65      0.10         MDD  143.2039 -33.65619
## 6 NSAMDD0006-56954     11.68      0.00         MDD  143.1665 -33.66432
```

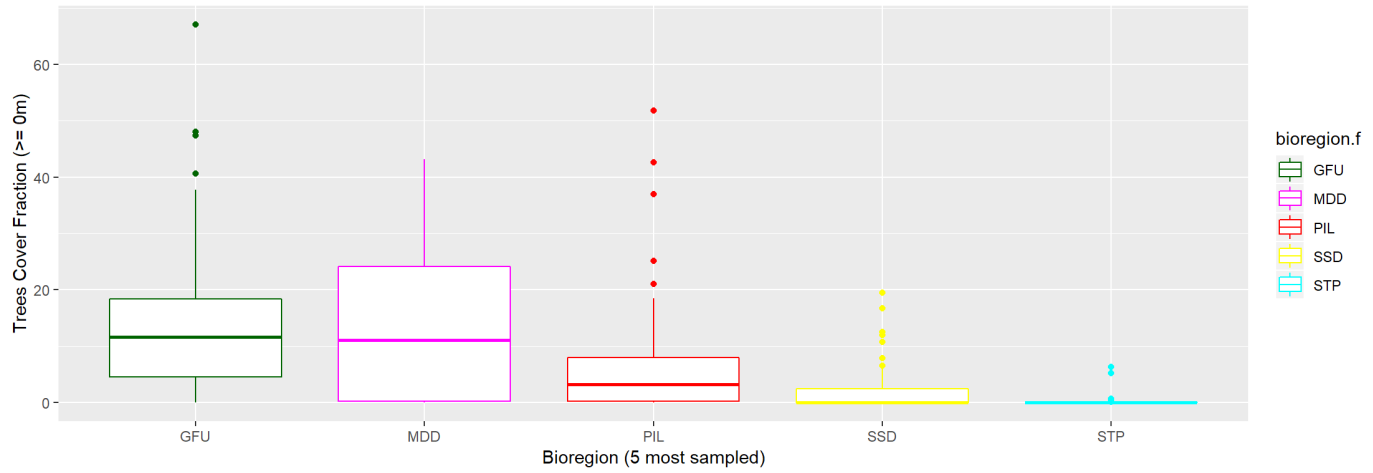
```
summary(AP.BioregTop5.VCF.df)
```

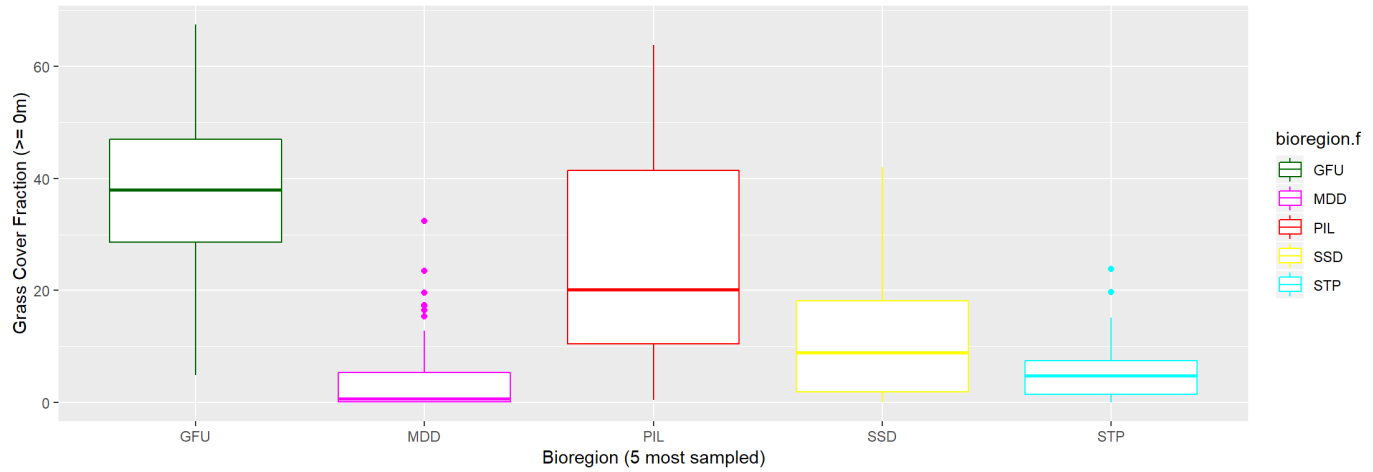
```
##            site_unique    VCF.trees        VCF.grass      bioregion.f
##  NSAMDD0001-56965:  1   Min.   : 0.000   Min.   : 0.000   GFU:41
##  NSAMDD0002-56952:  1   1st Qu.: 0.000   1st Qu.: 1.415   MDD:50
##  NSAMDD0003-56968:  1   Median : 1.190   Median : 9.700   PIL:35
##  NSAMDD0004-56953:  1   Mean   : 8.066   Mean   :16.420   SSD:46
##  NSAMDD0005-56969:  1   3rd Qu.:12.480   3rd Qu.:28.585   STP:38
##  NSAMDD0006-56954:  1   Max.   :67.030   Max.   :67.430
##  (Other)         :204
##    longitude        latitude
##  Min.   :117.0   Min.   :-35.00
##  1st Qu.:134.9   1st Qu.:-29.78
##  Median :136.8   Median :-25.12
##  Mean   :134.9   Mean   :-25.38
##  3rd Qu.:139.2   3rd Qu.:-21.88
##  Max.   :145.8   Max.   :-14.05
##
```

```
names(AP.BioregTop5.VCF.df)
```

```
## [1] "site_unique" "VCF.trees"   "VCF.grass"   "bioregion.f" "longitude"
## [6] "latitude"
```

```
# Graphical Visualisation
# =======================

# Trees: Boxplot
# --------------
AP.BioregTop5.VCF.trees =
ggplot(AP.BioregTop5.VCF.df, aes(x=bioregion.f, y=VCF.trees, color=bioregion.f)) +
geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(x="Bioregion (5 most sampled)", y = "Trees Cover Fraction (>= 0m)") +
theme(plot.title = element_text(hjust = 0.5))

# Grass: Boxplot
# --------------
AP.BioregTop5.VCF.grass =
ggplot(AP.BioregTop5.VCF.df, aes(x=bioregion.f, y=VCF.grass, color=bioregion.f)) +
geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(x="Bioregion (5 most sampled)", y = "Grass Cover Fraction (>= 0m)") +
theme(plot.title = element_text(hjust = 0.5))

# Plot both graphs
# ----------------
grid.arrange(AP.BioregTop5.VCF.trees, AP.BioregTop5.VCF.grass, nrow=2)
```






```
#grid.arrange(AP.BioregTop5.BA.trees, AP.BioregTop5.VCF.grass, ncol=2)
```

Subsetting by Taxonomy and Height

```
# Subsetting by Taxonomy and Height
# ********************************

# Compute Single Cover Values Tables
# ==================================
# Trees (by default my.growth_forms=c("Tree/Palm", "Tree Mallee"))
veg.cover.trees.gt5 = single_cover_value(AP.BioregTop5.l$veg.PI, by.growth_form=TRUE, my.grow
th_forms=c("Tree/Palm", "Tree Mallee"), min.height=5)

# These are the default values for the arguments of the function 'single_cover_value'
# So the following function call would produce exactly the same results
veg.cover.trees.gt5.2 = single_cover_value(AP.BioregTop5.l$veg.PI)
all.equal(veg.cover.trees.gt5, veg.cover.trees.gt5.2)
```

```
## [1] TRUE
```

```
rm(veg.cover.trees.gt5.2)


# Enrich DF
# =========

# Add: Bioregion, Longitude, Latitude
# -----------------------------------

# Both DF have different number of rows
dim(veg.cover.trees.gt5)
```

```
## [1] 210   2
```

```
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
AP.BioregTop5.VCF.trees.gt5.df  = merge(veg.cover.trees.gt5, AP.BioregTop5.l$site.info, by="s
ite_unique")[,c(names(veg.cover.trees.gt5), "bioregion.f", "longitude", "latitude")]
AP.BioregTop5.VCF.trees.gt5.df = na.omit(AP.BioregTop5.VCF.trees.gt5.df)
head(AP.BioregTop5.VCF.trees.gt5.df)
```

```
##        site_unique percentCover bioregion.f longitude  latitude
## 1 NSAMDD0001-56965         0.00         MDD  142.5602 -34.18392
## 2 NSAMDD0002-56952         3.56         MDD  142.6026 -34.20482
## 3 NSAMDD0003-56968         0.00         MDD  142.6041 -34.20754
## 4 NSAMDD0004-56953         8.51         MDD  142.5594 -34.16537
## 5 NSAMDD0005-56969         6.93         MDD  143.2039 -33.65619
## 6 NSAMDD0006-56954         8.22         MDD  143.1665 -33.66432
```

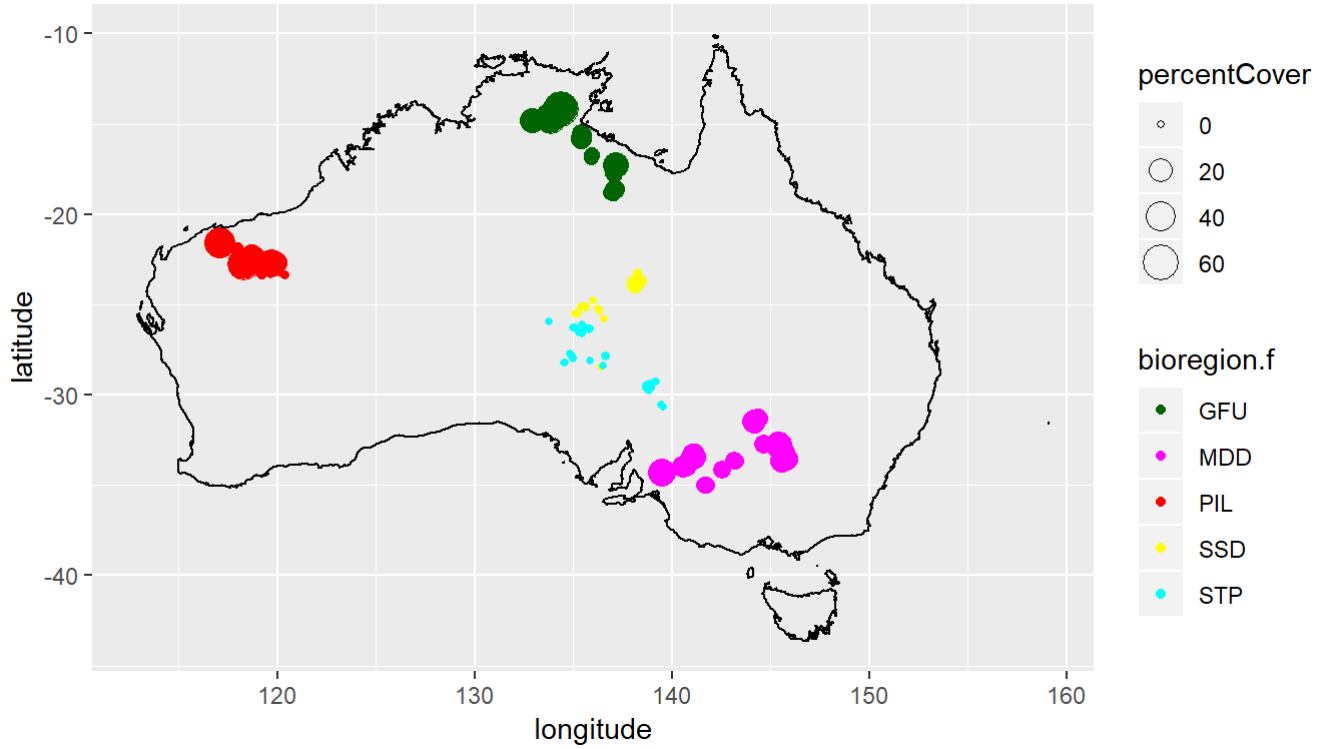
```
summary(AP.BioregTop5.VCF.trees.gt5.df)
```

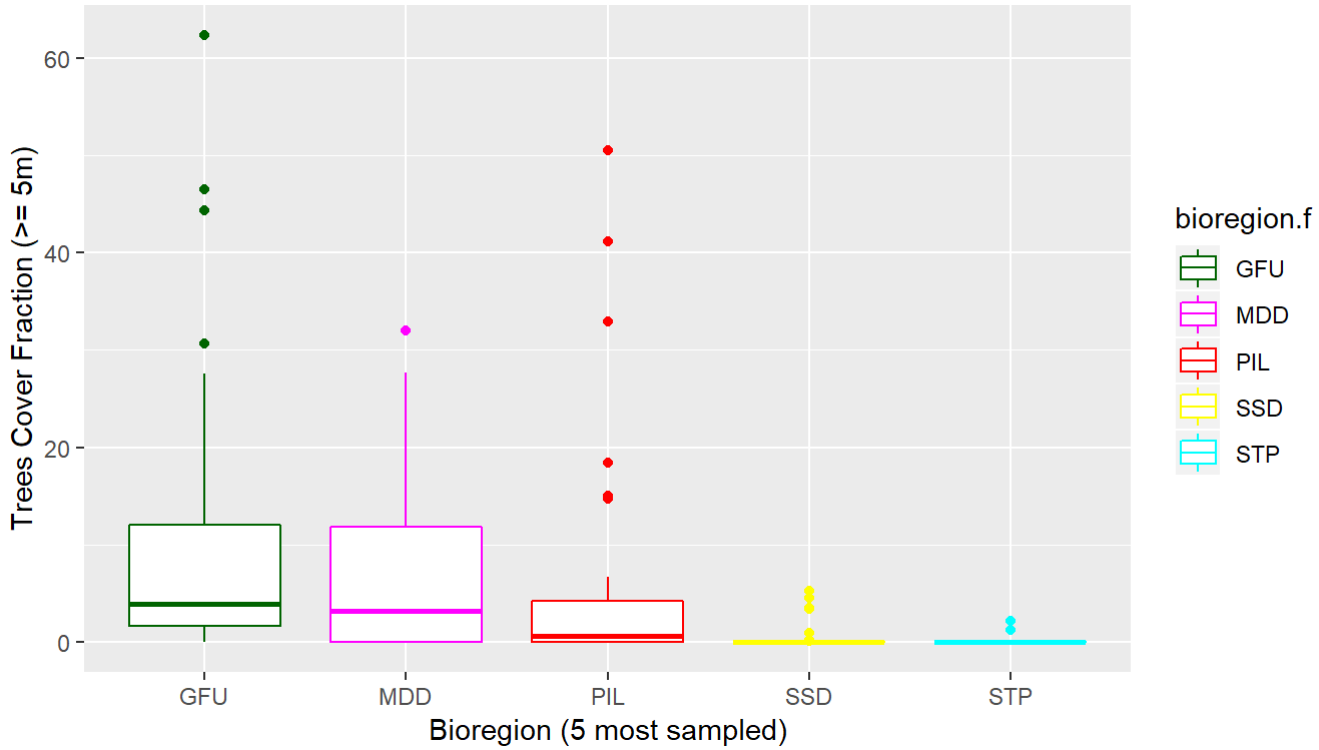
```
##            site_unique   percentCover    bioregion.f   longitude
##  NSAMDD0001-56965:  1   Min.   : 0.000   GFU:41      Min.   :117.0
##  NSAMDD0002-56952:  1   1st Qu.: 0.000   MDD:50      1st Qu.:134.9
##  NSAMDD0003-56968:  1   Median : 0.100   PIL:35      Median :136.8
##  NSAMDD0004-56953:  1   Mean   : 4.692   SSD:46      Mean   :134.9
##  NSAMDD0005-56969:  1   3rd Qu.: 4.550   STP:38      3rd Qu.:139.2
##  NSAMDD0006-56954:  1   Max.   :62.280               Max.   :145.8
##  (Other)         :204
##     latitude
##  Min.   :-35.00
##  1st Qu.:-29.78
##  Median :-25.12
##  Mean   :-25.38
##  3rd Qu.:-21.88
##  Max.   :-14.05
##
```

```
names(AP.BioregTop5.VCF.trees.gt5.df)
```

```
## [1] "site_unique"  "percentCover" "bioregion.f"  "longitude"
## [5] "latitude"
```

```
# Graphical Visualisation
# =======================

# Map with circle size = Percent Cover
# ------------------------------------
AP.BioregTop5.VCF.trees.gt5.p1 =
ggplot(data=AP.BioregTop5.VCF.trees.gt5.df, aes(x=longitude, y=latitude, colour=bioregion.f,
 fill=bioregion.f), alpha =0.5) +
geom_point(aes(size=percentCover), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# Boxplot
# -------
AP.BioregTop5.VCF.trees.gt5.p2 =
ggplot(AP.BioregTop5.VCF.trees.gt5.df, aes(x=bioregion.f, y=percentCover, color=bioregion.f))
+ geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(x="Bioregion (5 most sampled)", y = "Trees Cover Fraction (>= 5m)") +
theme(plot.title = element_text(hjust = 0.5))

# Plot both graphs
# ----------------
grid.arrange(AP.BioregTop5.VCF.trees.gt5.p1, AP.BioregTop5.VCF.trees.gt5.p2, nrow=2)
```






```
#grid.arrange(AP.BioregTop5.VCF.trees.gt5.p1, AP.BioregTop5.VCF.trees.gt5.p2, ncol=2)
```

BASAL AREA (OR NUMBER OF BASAL WEDGE HITS): `basal_area` function (for 5 most sampled bioregions).

The `basal_area` function calculates the Basal Area (or Number of Basal Wedge Hits) for each plot, using the raw basal wedge data returned by the `get_ausplots` funcion also in the `ausplotsR` package. This function returns a data frame with rows representing Plots (or species by plots) and a single column containning the Basal Area (m2/ha) or Hit Scores.

In this section we will:

- Compute the Basal Area for each plot (m2/ha) using the `basal_area` function.

- Enrich the data frame containing the Basal Area data with additional information (i.e. plot -Site-Visit-, bioregion, longitude, and latitude).
- Display Basal Areas on map of Australia (with Dots size proportional to Basal Area).
- Boxplot of Basal Areas by Bioregion.

```
# Calculate Basal Area
# ====================
AP.BioregTop5.BA = basal_area(AP.BioregTop5.l$veg.basal)
summary(AP.BioregTop5.BA)
```

```
##  site_unique        basal_area_m2_ha
##  Length:100         Min.   : 0.2857
##  Class :character   1st Qu.: 1.4556
##  Mode  :character   Median : 3.7833
##                     Mean   : 4.4884
##                     3rd Qu.: 5.5201
##                     Max.   :15.8000
```

```
head(AP.BioregTop5.BA)
```

```
##        site_unique basal_area_m2_ha
## 1 NSAMDD0002-56952         4.583333
## 2 NSAMDD0004-56953         4.805556
## 3 NSAMDD0005-56969         5.538889
## 4 NSAMDD0006-56954         4.077778
## 5 NSAMDD0007-56970         4.205556
## 6 NSAMDD0009-56971        14.694444
```

```
# Enrich DF
# =========
# Preparation
colnames(AP.BioregTop5.BA)
```

```
## [1] "site_unique"      "basal_area_m2_ha"
```

```
summary(AP.BioregTop5.BA)
```

```
##  site_unique        basal_area_m2_ha
##  Length:100         Min.   : 0.2857
##  Class :character   1st Qu.: 1.4556
##  Mode  :character   Median : 3.7833
##                     Mean   : 4.4884
##                     3rd Qu.: 5.5201
##                     Max.   :15.8000
```

```
head(AP.BioregTop5.BA)
```

```
##        site_unique basal_area_m2_ha
## 1 NSAMDD0002-56952         4.583333
## 2 NSAMDD0004-56953         4.805556
## 3 NSAMDD0005-56969         5.538889
## 4 NSAMDD0006-56954         4.077778
## 5 NSAMDD0007-56970         4.205556
## 6 NSAMDD0009-56971        14.694444
```

```
# Add: Bioregion, Longitude, Latitude
# ----------------------------------
# Both DF have different number of rows
dim(AP.BioregTop5.BA)
```

```
## [1] 100   2
```

```
dim(AP.BioregTop5.l$site.info)
```

```
## [1] 214  44
```

```
# Enrich with: Bioregion, Latitude, and Longitude
AP.BioregTop5.BA  = merge(AP.BioregTop5.BA, AP.BioregTop5.l$site.info, by="site_unique")[,c(n
ames(AP.BioregTop5.BA), "bioregion.f", "longitude", "latitude")]
AP.BioregTop5.BA = na.omit(AP.BioregTop5.BA)
head(AP.BioregTop5.BA)
```

```
##        site_unique basal_area_m2_ha bioregion.f longitude  latitude
## 1 NSAMDD0002-56952         4.583333         MDD  142.6026 -34.20482
## 2 NSAMDD0004-56953         4.805556         MDD  142.5594 -34.16537
## 3 NSAMDD0005-56969         5.538889         MDD  143.2039 -33.65619
## 4 NSAMDD0006-56954         4.077778         MDD  143.1665 -33.66432
## 5 NSAMDD0007-56970         4.205556         MDD  141.1608 -33.37998
## 6 NSAMDD0009-56971        14.694444         MDD  141.0655 -33.44049
```

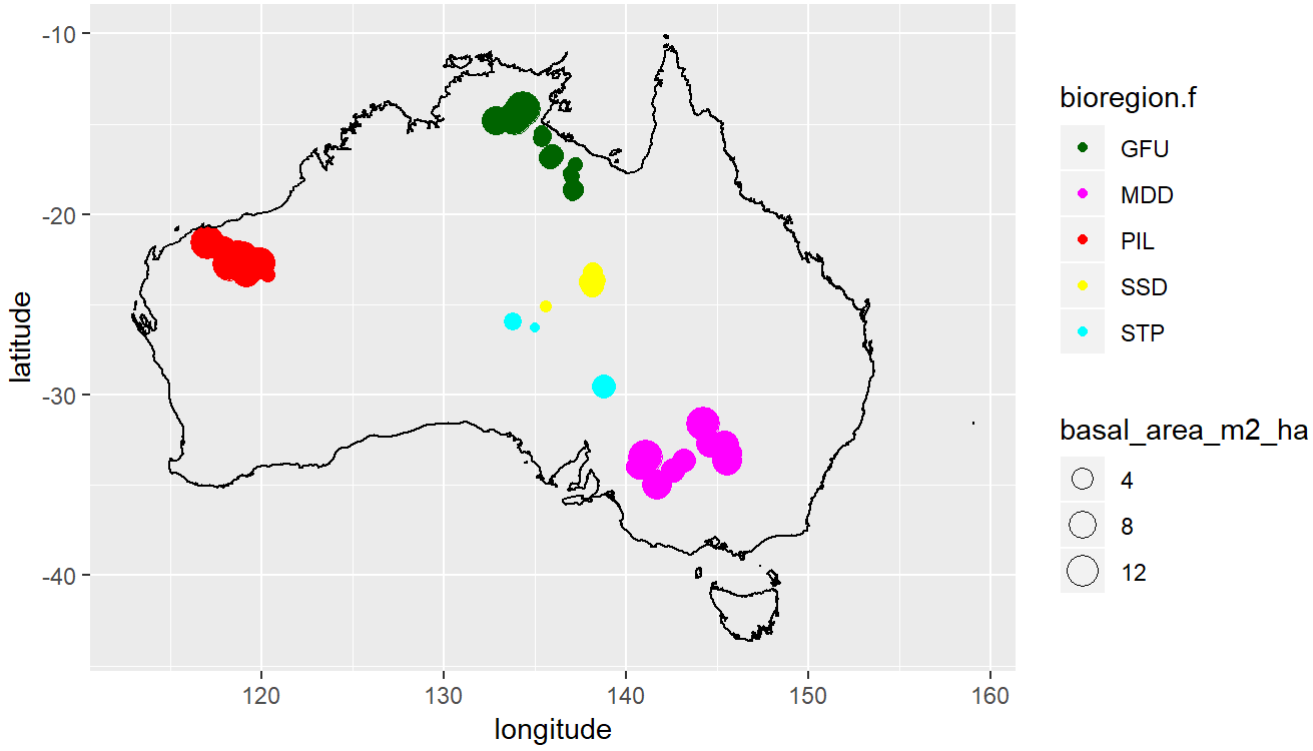
```
summary(AP.BioregTop5.BA)
```

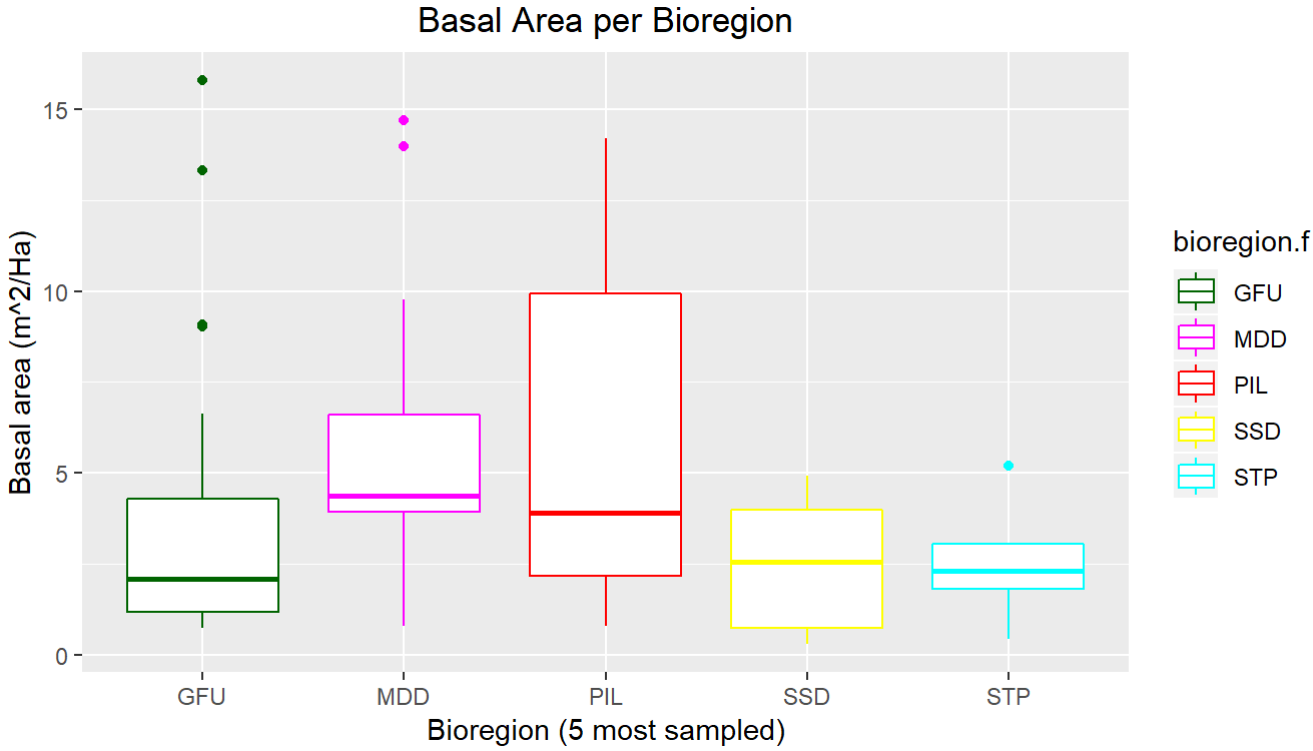
```
##  site_unique        basal_area_m2_ha  bioregion.f   longitude
##  Length:100         Min.   : 0.2857   GFU:34      Min.   :117.1
##  Class :character   1st Qu.: 1.4556   MDD:28      1st Qu.:129.8
##  Mode  :character   Median : 3.7833   PIL:25      Median :136.5
##                     Mean   : 4.4884   SSD: 9      Mean   :133.6
##                     3rd Qu.: 5.5201   STP: 4      3rd Qu.:140.6
##                     Max.   :15.8000               Max.   :145.8
##     latitude
##  Min.   :-35.00
##  1st Qu.:-31.61
##  Median :-22.63
##  Mean   :-23.75
##  3rd Qu.:-17.86
##  Max.   :-14.05
```

```
names(AP.BioregTop5.BA)
```

```
## [1] "site_unique"      "basal_area_m2_ha" "bioregion.f"
## [4] "longitude"        "latitude"
```

```
# Graphical Visualisation
# =======================

# Map with circle size = Basal Area (m2/ha)
# -----------------------------------------
AP.BioregTop5.BA.p1 =
ggplot(data=AP.BioregTop5.BA, aes(x=longitude, y=latitude, colour=bioregion.f, fill=bioregio
n.f), alpha =0.5) +
geom_point(aes(size=basal_area_m2_ha), pch=21) +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
geom_polygon(data=fortify(aus.sp), aes(x=long, y=lat, group=group), col="black", fill=NA)

# Boxplot
# -------
AP.BioregTop5.BA.p2 =
ggplot(AP.BioregTop5.BA, aes(x=bioregion.f, y=basal_area_m2_ha, color=bioregion.f)) +
geom_boxplot() +
scale_colour_manual(values = c("darkgreen", "magenta", "red", "yellow", "cyan")) +
scale_fill_manual(name="Bioregions (Top 5)", values = c("darkgreen", "magenta", "red", "yello
w", "cyan")) +
labs(title="Basal Area per Bioregion",x="Bioregion (5 most sampled)", y = "Basal area (m^2/H
a)") +
theme(plot.title = element_text(hjust = 0.5))

# Plot both graphs
# ----------------
grid.arrange(AP.BioregTop5.BA.p1, AP.BioregTop5.BA.p2, nrow=2)
```






```
#grid.arrange(AP.BioregTop5.BA.p1, AP.BioregTop5.BA.p2, ncol=2)
```