austraits:: CHEAT SHEET

austraits is an interface to traits.build databases, including AusTraits - Australia's Plant Trait Database. It enables users to download explore, visualise and extract relevant data from the database.

Download data

We recommend storing the AusTraits database in your project directory e.g. in a **data/austraits/** folder.

The **path** of this folder is important for loading the database into R without having to download the files again.

get_versions(path**)**
Retrieve all version information for the AusTraits database

date	doi	version
2024-05	10.5281/zenodo.11188867	**6.0.0**
2023-11	10.5281/zenodo.1015622	**5.0.0**

austraits ← load_austraits(doi/version, path**)**
Load specified version of the database into R environment. Note to assign database an object with ← operator

Structure

traits.build databases are **relational**. This means its data is organised in **13** tables as a **list** in R.

Names of the tables:
- traits
- locations
- contexts
- methods
- excluded_data
- taxonomic_updates
- taxa
- contributors
- sources
- definition
- schema
- metadata
- build_info

Every record in the database is linked to across tables by a unique combination of identifiers.

You can access each table using $

austraits$traits

austraits$contexts

Explore the data

Use the following functions to **explore** and **search** the database to get a sense of trait/taxonomic coverage.

summarise_database(database, trait_name/genus/family**)**
Compute summary statistics for traits/taxonomic group

summarise_database(database, "trait_name")

trait_name	n_records	n_dataset	n_taxa
leaf_area	22,764	95	4801
seed_germination_time	6037	2	2358
wood_density	10386	53	2002

Search for terms with exact/partial string matches in trait names/location properties/context properties

Functions returns vector of string matches

lookup_trait(database, trait name**)**
austraits |> lookup_trait("fruit")

lookup_locations_property(database, location property**)**
austraits |> lookup_location_property("temperature")

lookup_context_property(database, context_property**)**
austraits |> lookup_context_property("fire")

Extract data

Depending on input, functions returns a subset of the database or traits table

extract_trait(database, trait_name**)**
Extract data specific **trait name**
austraits |> extract_trait("leaf_area")

extract_dataset(database, dataset_id**)**
Extract specific **dataset**
austraits |> extract_dataset("Wenk_2022")

extract_taxa(database, taxon_name/genus/family**)**
Extract specific **taxa**
austraits |> extract_taxa(genus = "Acacia")

extract_data(database, table, col, col_value**)**
Extract data that meet specified criteria
austraits |> extract_data(contexts, context_property, "CO2")

Join data

Append information from other tables to the **traits** table.

Functions return traits table with added columns

join_location_coordinates(database**)**

join_location_properties(database, format = "single_column_pretty", vars = "all"**)**

join_contexts_properties(database, format = "single_column_pretty", vars = "all", include_description = TRUE**)**

join_methods(database, vars = c("methods")**)**

join_taxonomic_updates(database, vars = c("aligned_name")**)**

join_taxa(database, vars = c("family", "genus", "taxon_rank", "establishment_means")**)**

join_contributors(database, format = "single_column_pretty", vars = "all"**)**

flatten_database(database**)**
Consolidates information from all tables into a single wide table

bind_databases(database1, …**)**
Binds multiple databases into one

Reshape data

While the list structure of **austraits** retains all information, it may be more useful to condense the data down into a simpler format.

TRAIT VALUES

bind_trait_values(database $traits**)**
Concatenates trait values from measurements of the same observation into a string

separate_trait_values(database $traits**)**
Revert concatenated trait values back into multiple rows

## TABLES

trait_pivot_wider(database**)**
Distributes values in **trait name** as individual columns. Note some meta-data columns are excluded and this information is lost.

Visualise data

plot_trait_distribution_beeswarm(database, trait_name, y_axis_category, highlight=NA, hide_ids=FALSE**)**
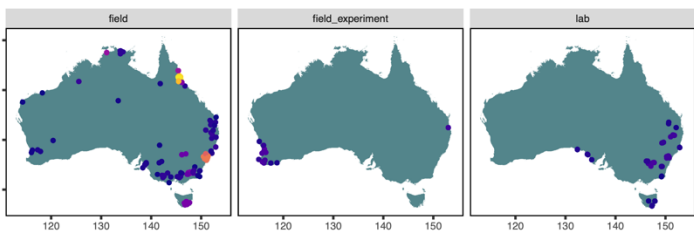Plot distribution of values for a given trait by table variable, genus or family

austraits |>
  extract_taxa("Myrtaceae") |>
  plot_trait_distribution_beeswarm(
  "stem_vessel_density","dataset_id",hide_ids= TRUE
)
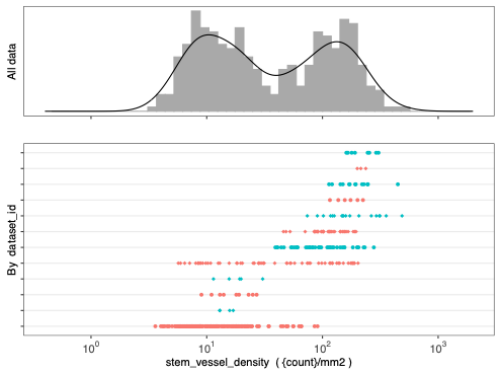
plot_locations(database, feature = "trait_name"**)**
Plot locations for a given feature of the database

austraits |>
  extract_trait("wood_density") |>
  plot_locations("basis_of_record")

Learn more
https://austraits.org/