

APCalign :: CHEAT SHEET

Wenk Elizabeth H., Cornwell William K., Fuchs Anne, Kar Fonti, Monro Anna M., Sauquet Hervé, Stephens Ruby E., Falster Daniel S. (2024) APCalign: an R package workflow and app for aligning and updating flora names to the Australian Plant Census. *Australian Journal of Botany* 72, BT24014.



APCalign uses the Australian Plant Census and the Australian Plant Name Index to align and update plant taxon names to current, accepted standards. It also provides useful information about diversity and establishment means of Australian plants across states.

Workflow

Aligning and updating your plant taxon names can be achieved in one simple step :

```
create_taxonomic_update_lookup(  
  taxa,  
  ...  
)
```

Vector of your
taxon names

Calling this **wrapper** function will :

1. **Retrieve** taxonomic reference lists (APC and APNI)

```
load_taxonomic_resources(...)
```



2. **Align** your taxon names to names in the APC and APNI using our match algorithms

```
align_taxa(...)
```



- Function will **first** attempt to align to names that exist in the **APC**
- If an alignment **cannot be found**, **APNI** will be used
- Includes **fuzzy/partial** string matches

2. **Update** aligned names to currently accepted names

```
update_taxonomy(...)
```



NOTE : We recommend calling each sub-function individually if you require finer control of each step's options

Data sources



Australian Plant Census (APC)

The **APC** is the national database of accepted names for Australian vascular plants. The APC provides information on:

- synonyms, and misapplications of scientific names
- establishment means (native/introduced)
- plant distribution across states and territories.

Australian Plant Name Index (APNI)

The **APNI** is a list for all Australian plants in scientific literature. It is used for standardising synonyms. APNI does not provide recommendations of taxonomy or nomenclature.

Retrieve data



Version-controlled taxonomic data are stored in our GitHub Repository at <https://github.com/traitecoevo/APCalign/releases>

Get all versions of **stable** taxonomic datasets

Function returns tibble of versions of taxonomic data

```
get_versions( )
```

versions
2024-10-11
2024-09-25
2024-07-31

Download either the **latest** taxonomic data or a **version-controlled** taxonomic dataset

Function returns list object of APC and APNI databases

Always
assign to an
object to
**use in other
functions**

```
resources <- load_taxonomic_resources(  
  stable_or_current_data = "stable",  
  version = "2024-09-25",  
  quiet = FALSE  
)
```

Align names



Find taxonomic or scientific name **matches** to the APC/APNI through standardizing formatting and fixing spelling errors

Function returns a tibble of original names and aligned names

```
alignments <- align_taxa(  
  original_name,  
  output = NULL,  
  full = FALSE,  
  resources = resources,  
  quiet = FALSE,  
  fuzzy_matches = TRUE,  
  fuzzy_abs_dist = 3,  
  fuzzy_rel_dist = 0.2,  
  imprecise_fuzzy_matches = FALSE,  
  APNI_matches = TRUE,  
  identifier = NA_character_  
)
```

Add **intermediary** fuzzy match columns to output

Use **fuzzy matching** or not for alignments

The **number** of characters allowed to **differ** for fuzzy match

The **proportion** of characters allowed to **differ** for fuzzy match

To use **APNI** in addition to APC for alignment

Add **identifiers** of your choice to informal names

Update names



Update name matched to accepted name in APC.

Function returns a tibble of original names, aligned names, accepted names and suggested names

Method to update names that are **ambiguous** due to taxonomic splits

```
update_taxonomy(  
  aligned_data = alignments,  
  taxonomic_splits = "most_likely_species",  
  quiet = TRUE,  
  output = NULL,  
  resources = resources  
)
```

Taxonomic splits

- "most_likely_species"

Returns the species name in use before the split; alternative names are returned in a separate column

- "return_all"

Adds additional rows to the output, one for each possible taxon concept

- "collapse_to_higher_taxon"

Returns the genus with possible names in square brackets.

Establishment Means

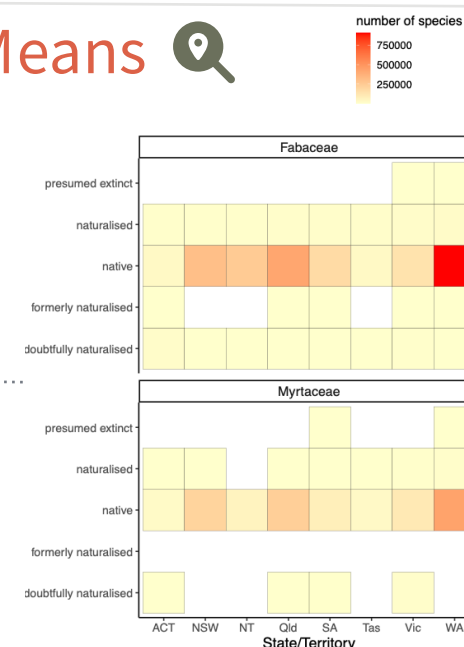


```
native_anywhere_in_australia(  
  species,  
  resources = resources  
)
```

Identify **establishment status** of taxon name

```
state_diversity_counts(  
  state,  
  resources = resources  
)
```

Summarise **counts** of establishment means by **state**



Learn more



Don't want to code? No worries!
Try our **Shiny** interface:
<https://unsw.shinyapps.io/APCalign-app/>

Read our published paper here!

