

APCalign :: CHEAT SHEET



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 resources from APC and APNI

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



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

```
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

3. **Update** your taxon names in a transparent and reproducible manner

```
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 them
- established means (native/introduced)
- plant distribution across states and territories.

Australian Plant Name Index (APNI)

The **APNI** is a database 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
#> # A tibble: 3 x 1
#>   versions
#>   <date>
#> 1 2024-10-11
#> 2 2024-09-25
#> 3 2024-07-31
```

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

Function returns list object of APC and APNI databases

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

Always assign to an object to use in other functions

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_  
)
```

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

Coarse level fuzzy matching for more alignments

Update names



Update name matches to APC/APNI standards

Function returns a tibble of original names, aligned 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"

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

- "collapse_to_higher_taxon"

Returns the genus rank of the taxon name

Establishment Means



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

Identify **establishment status** of aligned name

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

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



Don't want to code? No worries! Try our **Shiny** interface:

<https://unsw.shinyapps.io/APCalign-app/>

Read our published paper here!



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Installation

Stable release from **CRAN** :

```
install.packages("APCalign")
```

Development version from **GitHub** :

```
remotes::install_github("traitecoevo/APCalign")
```

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```

Taxonomic splits

- "most_likely_species"
Returns the species name in use before the split; alternative names are returned in a separate column
- "return_all"
Returns the taxon name in use before the split; alternative names are returned in a separate column
- "collapse_to_higher_taxon"
Returns the genus rank of the taxon name

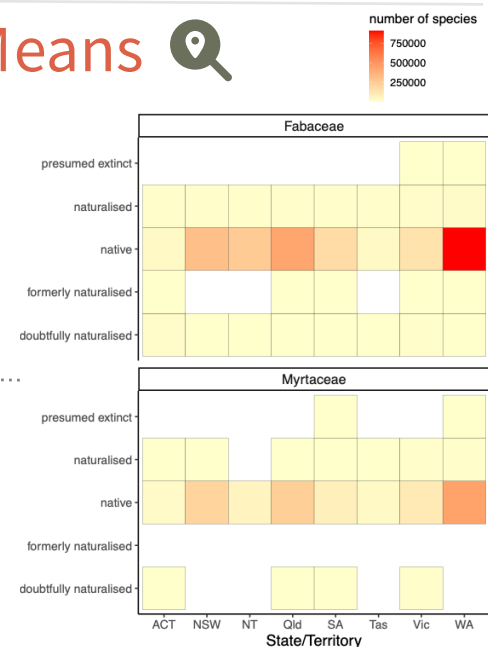
Establishment Means

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Identify **establishment status** of aligned name

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