# Package: taxonomy.tools (via r-universe)

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**Description** Tools to Work with Taxonomic Data.

**License** GPL (>= 3)

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**URL** https://github.com/Pakillo/taxonomy.tools, https://pakillo.github.io/taxonomy.tools/

**BugReports** https://github.com/Pakillo/taxonomy.tools/issues

**Imports** dplyr, future, future.apply, rWCVP (>= 1.2.6), tidyr, utils

**Suggests** rWCVPdata, testthat (>= 3.0.0)

**Remotes** matildabrown/rWCVPdata, matildabrown/rWCVP

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## Contents

wcvp_match_names_parallel *Parallelised matching of plant taxonomic names against WCVP*

## Description

Parallelised version of `rWCVP::wcvp_match_names()` to check plant taxonomic names against the World Checklist of Vascular Plants (WCVP), using `future.apply::future.apply()`.

## Usage

```
wcvp_match_names_parallel(
  df = NULL,
  name_col = NULL,
  author_col = NULL,
  fuzzy = TRUE,
  plan = "multisession",
  cores = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| df | Data frame containing taxonomic names to be matched against WCVP. |
| name_col | Character. The column in 'df' containing the taxon names for matching. |
| author_col | Character. The column in 'df' that has the name authority, to aid matching. Set to NULL to match with no author string. |
| fuzzy | Logical; whether or not fuzzy matching should be used for names that could not be matched exactly. |
| plan | Character. Name of a `future::plan()` to be used for parallelisation. Recommended plan is "multisession". Use "sequential" for non-parallel processing. |
| cores | Number of cores to use in parallel. |
| ... | Further arguments to be passed to `rWCVP::wcvp_match_names()` |

## Value

A data frame

## Examples

```
## Not run:
df <- data.frame(taxon = c("Laurus nobilis", "Laurus nobilis", "Laurus nobili"),
                 author = c(NA, "L.", NA))
out <- wcvp_match_names_parallel(df, name_col = "taxon", author_col = "author",
  cores = 3)

## End(Not run)
```

wcvp_resolve_multiple_matches *Resolve multiple matches in WCVP*

## Description

This function tries to resolve automatically the cases of multiple matches found after running a vector of taxonomic names against the World Checklist of Vascular Plants (WCVP).

## Usage

```
wcvp_resolve_multiple_matches(df = NULL, name_col = NULL)
```

## Arguments

| | |
|---|---|
| df | Data frame with matching results, as produced by rWCVP::wcvp_match_names() or wcvp_match_names_parallel() |
| name_col | Character. Name of the column in 'df' containing the taxon names. |

## Value

A data frame

## Author(s)

Adapted from rWCVP vignette

## See Also

https://matildabrown.github.io/rWCVP/articles/redlist-name-matching.html

## Examples

```
## Not run:
df <- data.frame(taxon = "Acacia dealbata")
matching <- wcvp_match_names_parallel(df, name_col = "taxon")
out <- wcvp_resolve_multiple_matches(matching, name_col = "taxon")

## End(Not run)
```

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