

Package ‘Rcompadre’

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Type Package

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Description

Utility functions for interacting with the 'COMPADRE' and 'COMADRE' databases of matrix population models. Described in Jones et al. (2021) <doi:10.1101/2021.04.26.441330>.

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URL <https://github.com/jonesor/Rcompadre>

BugReports <https://github.com/jonesor/Rcompadre/issues>

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'CompadreDB-Subsetting.R' 'CompadreDB-Tidyverse.R'
'CompadreMat.R' 'ClassUnionMethods.R' 'cdb_check_species.R'
'cdb_collapse.R' 'cdb_compare.R' 'cdb_fetch.R' 'cdb_flag.R'
'cdb_flatten.R' 'cdb_id.R' 'cdb_id_stages.R' 'cdb_id_studies.R'
'cdb_mean_matF.R' 'cdb_metadata.R' 'cdb_rbind.R'
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as_cdb	<i>Convert legacy COM(P)ADRE database object to CompadreDB</i>
--------	--

Description

Convert a legacy COM(P)ADRE database object (of class 'list') to a CompadreDB object.

Usage

```
as_cdb(from)
```

Arguments

from A legacy COM(P)ADRE database

Value

A CompadreDB object

Author(s)

Iain M. Stott

Examples

```
Compadre <- as_cdb(CompadreLegacy)
```

cdb_check_species	<i>Check whether a COM(P)ADRE database contains one or more species of interest</i>
-------------------	---

Description

Takes a vector of species names and checks whether those species are represented within a CompadreDB object. It outputs either a data frame depicting the species of interest and whether they occur in the database (TRUE/FALSE), or, if `return_db == TRUE`, a CompadreDB object subset to the species of interest.

Usage

```
cdb_check_species(cdb, species, return_db = FALSE)
```

Arguments

<code>cdb</code>	A CompadreDB object
<code>species</code>	Character vector of binomial species names, with the genus and specific epithet separated by either an underscore or a space (e.g. <code>c("Acipenser_fulvescens", "Borrelia_burgdorferi")</code>)
<code>return_db</code>	Logical argument indicating whether a database should be returned

Value

If `return_db == FALSE`, returns a data frame with a column of species names and a column indicating whether a species occurs in the database. If `return_db == TRUE`, returns a subset of `cdb` containing only those species within argument `species`.

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See Also

Other data checking: [cdb_collapse\(\)](#), [cdb_compare\(\)](#), [cdb_flag\(\)](#), [mpm_methods](#)

Examples

```
species <- c("Primula vulgaris", "Trillium ovatum", "Homo sapiens")
cdb_check_species(Compadre, species)
CompadreSubset <- cdb_check_species(Compadre, species, return_db = TRUE)
```

<code>cdb_collapse</code>	<i>Collapse a COM(P)ADRE database by averaging matrices over levels of one or more grouping variables</i>
---------------------------	---

Description

Collapses a CompadreDB object by averaging matrices over levels of one or more grouping variables (e.g. `SpeciesAuthor`, `MatrixPopulation`).

For a given study and species, a COM(P)ADRE database may contain multiple matrices, reflecting different combinations of population, year, and/or treatment. Collapsing allows a user to obtain a single 'grand mean matrix' for each group of interest (e.g. `MatrixPopulation`), and therefore limit pseudoreplication.

All members of a group *must* have the same matrix dimension (consider adding `MatrixDimension` as a grouping variable). All members of a group *should* have the same `AnnualPeriodicity` and matrix stage class definitions (see [cdb_id_stages](#)). Note that Seasonal matrices should not be collapsed using this method (they should be matrix-multiplied rather than averaged).

Usage

```
cdb_collapse(cdb, columns)
```

Arguments

cdb	A CompadreDB object
columns	Vector of grouping variables to collapse over (corresponding to columns within cdb)

Details

Will give a warning if members of any group do not all share the same AnnualPeriodicity or stage class definitions, or if cdb contains any rows with a MatrixComposite value of "Seasonal".

Prior to collapsing, columns of class 'factor' will be coerced to 'character', and any list-column apart from mat will be removed.

Within a group, rows of a given column are collapsed as follows:

- mat: matrices are averaged using [mpm_mean](#), and stage class definitions are taken from the first group member
- MatrixComposite: return original value if N = 1, else return "Collapsed"
- Lat: re-calculated by averaging Lat column (if available)
- Lon: re-calculated by averaging Lon column (if available)
- SurvivalIssue: re-calculated from the collapsed mat ($\max(\text{colSums}(\text{matU}))$)
- others: if all elements equal return that unique value, else paste together all unique values separated by ";"

Value

A CompadreDB object

Author(s)

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See Also

[cdb_id_stages](#)

Other data checking: [cdb_check_species\(\)](#), [cdb_compare\(\)](#), [cdb_flag\(\)](#), [mpm_methods](#)

Examples

```
# filter out Seasonal matrices
CompSub <- subset(Compadre, MatrixComposite != "Seasonal")

# add column identifying unique stage class definitions
CompSub$id_stage <- cdb_id_stages(CompSub, "MatrixClassOrganized")

# collapse
CompCollapse <- cdb_collapse(CompSub, columns = c("id_stage"))
```

 cdb_compare

Compare two versions or subsets of a COM(P)ADRE database

Description

Prints a summary of the differences between two CompadreDB objects, including the number of species, studies, and matrices in each. If argument `verbose == TRUE`, additionally prints a list of the species and studies that are present in one database but not the other.

Usage

```
cdb_compare(cdb1, cdb2, verbose = FALSE)
```

Arguments

<code>cdb1, cdb2</code>	CompadreDB objects to compare
<code>verbose</code>	Logical argument indicating whether or not to return lots of detail

Value

NULL. Output is printed rather than returned.

Author(s)

Owen R. Jones <jones@biology.sdu.dk>

See Also

Other data checking: [cdb_check_species\(\)](#), [cdb_collapse\(\)](#), [cdb_flag\(\)](#), [mpm_methods](#)

Examples

```
Compadre1 <- subset(Compadre, Continent == "Asia")
Compadre2 <- subset(Compadre, Continent == "Africa")

cdb_compare(Compadre1, Compadre2)
```

cdb_fetch	<i>Fetch the COM(P)ADRE database from compadre-db.org or a local file</i>
-----------	---

Description

Fetches the current version of a COM(P)ADRE database from <https://compadre-db.org>, or load any version stored in a local .RData file.

Usage

```
cdb_fetch(cdb)
```

Arguments

cdb	Either "comadre" or "compadre" (case insensitive) to fetch the most recent database from https://compadre-db.org , or a path to an existing COMPADRE database (i.e. .RData file) stored on the local machine.
-----	---

Value

A CompadreDB object

Author(s)

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See Also

Other data acquisition: [cdb_metadata\(\)](#)

Examples

```
## Not run:  
#Download direct from the COMPADRE website  
compadre <- cdb_fetch("compadre")  
  
#using file path to downloaded data  
compadre <- cdb_fetch("data/COMPADRE_v.5.0.1.RData")  
  
## End(Not run)
```

 cdb_flag

Flag potential issues in matrices of a COM(P)ADRE database

Description

Adds columns to the data slot of a CompadreDB object that flag potential problems in the matrix population models. These columns can subsequently be used to subset the database by logical argument.

Optional checks include:

- check_NA_A: missing values in matA?
- check_NA_U: missing values in matU?
- check_NA_F: missing values in matF?
- check_NA_C: missing values in matC?
- check_zero_U: matU all zeros (including NA)?
- check_singular_U: matU singular (i.e. non-invertable)?
- check_component_sum: do matU/matF/matC components sum to matA (see *Details*)?
- check_ergodic: is matA ergodic (see [isErgodic](#))?
- check_irreducible: is matA irreducible (see [isIrreducible](#))?
- check_primitive: is matA primitive (see [isPrimitive](#))?
- check_surv_gte_1: does matU contains values that are equal to or greater than 1?

Usage

```

cdb_flag(
  cdb,
  checks = c("check_NA_A", "check_NA_U", "check_NA_F", "check_NA_C", "check_zero_U",
    "check_singular_U", "check_component_sum", "check_ergodic", "check_irreducible",
    "check_primitive", "check_surv_gte_1")
)

```

Arguments

cdb	A CompadreDB object
checks	Character vector specifying which checks to run. Defaults to all, i.e. <code>c("check_NA_A", "check_NA_U", "check_NA_F", "check_NA_C", "check_zero_U",</code>

Details

For the flag `check_component_sum`, a value of NA will be returned if the matrix sum of `matU`, `matF`, and `matC` consists only of zeros and/or NA, indicating that the matrix has not been split.

Value

Returns cdb with extra columns appended to the data slot (columns have the same names as the corresponding elements of checks) to indicate (TRUE/FALSE) whether there are potential problems with the matrices corresponding to a given row of the data.

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See Also

Other data checking: [cdb_check_species\(\)](#), [cdb_collapse\(\)](#), [cdb_compare\(\)](#), [mpm_methods](#)

Examples

```
CompadreFlag <- cdb_flag(Compadre)

# only check whether matA has missing values, and whether matA is ergodic
CompadreFlag <- cdb_flag(Compadre, checks = c("check_NA_A", "check_ergodic"))
```

cdb_flatten	<i>Convert a COM(P)ADRE database to a flat data frame with matrices and vectors stored in string representation</i>
-------------	---

Description

Converts a CompadreDB object to a flat data frame by extracting the data slot, and splitting the mat column into separate columns for each component (matrices matA, matU, matF, matC, and vectors MatrixClassAuthor, and MatrixClassOrganized). The component matrices and vectors within the six new columns are stored in string format so that the database can be written to a flat file format such as csv (see [string_representation](#)).

Usage

```
cdb_flatten(cdb)
```

Arguments

cdb A CompadreDB object

Value

A data frame based on the data slot of `cdb`, but with the column `mat` replaced by six separate columns (for matrices `matA`, `matU`, `matF`, `matC`, and vectors `MatrixClassAuthor`, and `MatrixClassOrganized`), whose elements are matrices or vectors in string representation.

Author(s)

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See Also

[cdb_unflatten](#) [string_representation](#)

Other data management: [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
CompadreFlat <- cdb_flatten(Compadre)
```

cdb_id	<i>Create integer identifiers for a COM(P)ADRE database corresponding to unique combinations of a given set of columns</i>
--------	--

Description

Creates a vector of integer identifiers corresponding to the rows of a `CompadreDB` object, based on unique combinations of the elements in a given set of columns.

Usage

```
cdb_id(cdb, columns)
```

Arguments

cdb	A <code>CompadreDB</code> object
columns	Vector of column names from which unique combinations should be identified

Details

Identifiers are assigned by pasting together the relevant columns, assigning factor levels based on alphabetical order, and then converting the factor levels to integers.

Value

Vector of integer identifiers corresponding to the rows of `cdb`, based on unique combinations of the elements in columns.

Author(s)

Patrick Barks <patrick.barks@gmail.com>

See Also

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
cdb_id(Compadre, columns = c("SpeciesAuthor", "MatrixTreatment"))
```

cdb_id_stages	<i>Create integer identifiers for a COM(P)ADRE database corresponding to unique combinations of species and matrix stage class definitions</i>
---------------	--

Description

Creates a vector of integer identifiers corresponding to the rows of a CompadreDB object, based on unique combinations of the column 'SpeciesAccepted' and a list of matrix stage class definitions (either 'MatrixClassAuthor' or 'MatrixClassOrganized').

Usage

```
cdb_id_stages(cdb, stage_def = "MatrixClassAuthor")
```

Arguments

cdb	A CompadreDB object
stage_def	Whether to define matrix stage class based on "MatrixClassAuthor" or "Matrix-ClassOrganized" (see <i>Details</i>). Defaults to "MatrixClassAuthor".

Details

The vector 'MatrixClassOrganized' reflects standardized stage classes ('prop', 'active', or 'dorm'), whereas 'MatrixClassAuthor' reflects a description of the stage classes as defined by the original author (e.g. `c('Seedling', 'Medium rosette', 'Large (2 rosettes)', 'Flowering')`).

Because the 'MatrixClassAuthor' definitions are less standardized, they are more prone to typos that could lead to slight differences between stage descriptions of matrices that really do have the same stage classes (e.g. a set of matrices from a single study/species/population). Therefore, using 'MatrixClassAuthor' to define stage classes is potentially prone to mistakenly 'splitting' identifiers that should really be the same.

'MatrixClassOrganized' has the opposite problem. It's possible for two matrices from a given study to have the same stage definitions based on 'MatrixClassOrganized', but legitimately differ in stage definitions as defined by the author. Therefore, using 'MatrixClassAuthor' to define stage classes is potentially prone to mistakenly 'lumping' identifiers that should actually differ.

Because the majority of studies in COM(P)ADRE use a single set of stage definitions for all matrices, and typos are rare, results for the different stage definitions will usually be similar. Note, however, that the actual integers returned for the different stage definitions are likely to be very different (because they are based on alphabetical order).

Value

Vector of integer identifiers corresponding to the rows of cdb.

Author(s)

Patrick Barks <patrick.barks@gmail.com>

See Also

[cdb_id](#)

Other data management: [cdb_flatten\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
cdb_id_stages(Compadre, stage_def = "MatrixClassOrganized")
```

cdb_id_studies	<i>Create a vector of unique study identifiers from a COM(P)ADRE database</i>
----------------	---

Description

Creates a vector of integer study identifiers corresponding to the rows of a CompadreDB object, based on unique combinations of the columns 'Authors', 'Journal', 'YearPublication', and 'DOI.ISBN' (or optionally, a different set of columns supplied by the user).

Usage

```
cdb_id_studies(  
  cdb,  
  columns = c("Authors", "Journal", "YearPublication", "DOI.ISBN")  
)
```

Arguments

cdb	A CompadreDB object
columns	Vector of column names from which unique combinations should be identified. Defaults to c("Authors", "Journal", "YearPublication", "DOI.ISBN").

Details

Identifiers are assigned by pasting together the relevant columns, assigning factor levels based on alphabetical order, and then converting the factor levels to integers.

Value

Vector of integer study identifiers corresponding to the rows of cdb, based on unique combinations of the elements in columns.

Author(s)

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See Also

[cdb_id](#)

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
Compadre$StudyID <- cdb_id_studies(Compadre)
```

cdb_mean_matF	<i>Calculate a population-specific mean fecundity matrix for each set of matrices in a COM(P)ADRE database</i>
---------------	--

Description

Takes a CompadreDB object and calculates a grand mean fecundity matrix for each unique population (a mean of all population-specific fecundity matrices, including fecundity matrices for which `MatrixComposite == 'Mean'`).

Populations are defined based on unique combinations of the columns 'SpeciesAuthor', 'Matrix-Population', and 'MatrixDimension', (or optionally, a different set of columns supplied by the user).

The main purpose of this function is to identify stage classes that are *potentially* reproductive (i.e. the absence of fecundity in a given stage class and year does not necessarily indicate that the stage in question is non-reproductive).

Usage

```
cdb_mean_matF(  
  cdb,  
  columns = c("SpeciesAuthor", "MatrixPopulation", "MatrixDimension")  
)
```

Arguments

`cdb` A CompadreDB object

`columns` Vector of column names from which unique populations should be identified. Defaults to `c("SpeciesAuthor", "MatrixPopulation", "MatrixDimension")`.

Value

Returns a list of matrices, representing the mean fecundity matrix associated with each row of the database.

Author(s)

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See Also

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
# print matF associated with row 16 of database
Compadre$mat[[16]]

# create list of meanMatFs
meanF <- cdb_mean_matF(Compadre)

# print meanMatF associated with row 16 of database
meanF[[16]]
```

`cdb_metadata`

Extract metadata from a COM(P)ADRE database

Description

Extract a tibble with only metadata information from a CompadreDB object, by dropping the matrix column "mat".

Usage

```
cdb_metadata(cdb)
```

Arguments

cdb A CompadreDB object

Details

Transforms the large CompadreDB object into a tibble and drops the matrix column ("mat").

Value

Tibble with all metadata columns of cdb

Author(s)

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See Also

Other data acquisition: [cdb_fetch\(\)](#)

Examples

```
Compadre_metadata <- cdb_metadata(Compadre)
```

cdb_rbind

Merge two COM(P)ADRE databases via row-bind

Description

Merges two CompadreDB objects via a row-bind of the data slots.

Usage

```
cdb_rbind(cdb1, cdb2)
```

Arguments

cdb1, cdb2 CompadreDB objects

Value

A CompadreDB object created by binding the rows of cdb1 and cdb2

Author(s)

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Owen R. Jones <jones@biology.sdu.dk>

See Also

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
Compadre1 <- subset(Compadre, Continent == "Asia")
Compadre2 <- subset(Compadre, Continent == "Africa")

cdb_rbind(Compadre1, Compadre2)
```

cdb_unflatten	<i>Reconstitute a flattened COM(P)ADRE database (created by cdb_flatten) as a CompadreDB object</i>
---------------	---

Description

Converts a flattened COM(P)ADRE database (created by [cdb_flatten](#)) back to the CompadreDB class

Usage

```
cdb_unflatten(db)
```

Arguments

db A data frame created with [cdb_flatten](#), with columns for matrices matA, matU, matF, matC, and vectors MatrixClassAuthor, and MatrixClassOrganized in string representation.

Value

A CompadreDB object. Because version details are lost when the database is flattened, the Version and DateCreated elements of the returned CompadreDB object will be NA.

Author(s)

Patrick M. Barks <patrick.barks@gmail.com>

See Also

[cdb_flatten](#) [string_representation](#)

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
CompadreFlat <- cdb_flatten(Compadre) # flatten
Compadre2 <- cdb_unflatten(CompadreFlat) # reconstitute
```

cdb_unnest	<i>Unnest a COM(P)ADRE database by spreading the components of CompadreMat into separate list-columns</i>
------------	---

Description

Unnests a CompadreDB object by spreading the components of CompadreMat into separate list-columns. Components that may be extracted include:

- matA (matrix)
- matU (matrix)
- matF (matrix)
- matC (matrix)
- MatrixClassAuthor (character vector)
- MatrixClassOrganized (character vector)
- MatrixClassNumber (integer vector)

Usage

```
cdb_unnest(
  cdb,
  components = c("matA", "matU", "matF", "matC", "MatrixClassAuthor",
    "MatrixClassOrganized", "MatrixClassNumber")
)
```

Arguments

cdb	A CompadreDB object
components	Character vector specifying which components to extract. Defaults to all, i.e. c("matA", "matU", "matF", "matC", "MatrixClassAuthor", "MatrixClassOrganized")

Value

cdb with additional list-columns for each element of argument components

Author(s)

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See Also

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [mpm_mean\(\)](#), [string_representation](#)

Examples

```
# unnest all components
CompadreUnnest <- cdb_unnest(Compadre)

# unnest select components (matU and MatrixClassAuthor)
CompadreUnnest <- cdb_unnest(Compadre, c("matU", "MatrixClassAuthor"))
```

Compadre	<i>Subsamples of the COMPADRE Plant Matrix Database and COMADRE Animal Matrix Database for testing and examples</i>
----------	---

Description

Compadre (plant matrices) and Comadre (animal matrices) are subsamples of the COMPADRE Plant Matrix Database and COMADRE Animal Matrix Database, respectively, that are used for testing and examples. Each object is of class 'CompadreDB' and therefore has the following two slots: data and version.

For full documentation see the [COMPADRE User Guide](#).

Usage

Compadre

Comadre

Format

Slot **data** - A tibble-style data frame with the following 48 columns:

- mat - A list of 'CompadreMat' objects, each with the following slots:
 - matA - A matrix population model
 - matU - The survival- and growth-related component of matA
 - matF - The sexual reproduction component of matA
 - matC - The clonal reproduction component of matA
 - matrixClass - A data frame with the following columns:
 - * MatrixClassOrganized - Standardized stage class of the matrix population model
 - * MatrixClassAuthor - Stage description from the original publication
 - * MatrixClassNumber - Integer stage number
- SpeciesAuthor - Binomial species name given by the paper's author

- SpeciesAccepted - Accepted binomial species name taken from *The Plant List* or *Catalogue of Life*
- CommonName - Common name for species used in the publication
- Genus - Taxonomic genus that the accepted species belongs to
- Family - Family that the species belongs to
- Order - Order that the species belongs to
- Class - Class that the species belongs to
- Phylum - Phylum that the species belongs to
- Kingdom - Kingdom that the species belongs to
- OrganismType - Organism type (see COMPADRE User Guide for documentation)
- DicotMonoc - Whether the species is a dicot or monocot. Non-angiosperms are NA.
- AngioGymno - Whether the species is an angiosperm or gymnosperm. Non-plants are NA.
- Authors - Last name of all authors (separated with ";")
- Journal - Abbreviated journal title, or type of source document (e.g. "PhD thesis")
- YearPublication - Year of publication
- DOI.ISBN - Digital Object Identifier or International Standard Book Number codes to identify each publication
- AdditionalSource - Additional source(s) used to reconstruct the matrix or obtain additional metadata for the matrix (if applicable)
- StudyDuration - Number of years of observation in study (StudyEnd - StudyStart)
- StudyStart - Study start year
- StudyEnd - Study end year
- AnnualPeriodicity - Inverse of the length of the projection interval (in years)
- NumberPopulations - The number of study populations as defined by the authors. Within site replication of permanent plots is not defined as separate populations
- MatrixCriteriaSize - Indicates whether the matrix contains stages based on size. If so, indicates what that measure of size is
- MatrixCriteriaOntogeny - Indicates whether the matrix contains stages based on ontogenic/developmental stages
- MatrixCriteriaAge - Indicates whether the matrix contains stages based on age
- MatrixPopulation - Population name or definition of where the matrix was recorded, usually given by the author. See COMPADRE User Guide.
- Lat - Latitude in decimal degrees
- Lon - Longitude in decimal degrees
- Altitude - Altitude of study site (m above sea level)
- Country - 3-letter ISO country code for the country in which the study took place (multiple countries separated with ";")
- Continent - Continent on which study took place
- Ecoregion - Ecoregion in which study took place. See COMPADRE User Guide.

- StudiedSex - Whether study included only males ("M"), only females ("F"), or both sexes ("M/F")
- MatrixComposite - Indicates the type of matrix population model. Possible values are Individual, Mean, Pooled, and Seasonal. See COMPADRE User Guide.
- MatrixTreatment - Describes if a treatment was applied to the population or not. If yes, includes a brief description of the treatment. If not, Unmanipulated
- MatrixCaptive - Whether species was studied in the wild (W), captivity (C), or captured from a wild population (CW)
- MatrixStartYear - First year of matrix
- MatrixStartSeason - First season of matrix as described by author (hemisphere-specific)
- MatrixStartMonth - First month of matrix
- MatrixEndYear - Final year of matrix
- MatrixEndSeason - Final season of matrix as described by author (hemisphere-specific)
- MatrixEndMonth - Final month of matrix
- MatrixSplit - Whether the **A** matrix has been split into components **U**, **F**, and **C** ("Divided") or not ("Indivisible"). If not, elements of matU, matF, and matC are filled with NA
- MatrixFec - Whether fecundity was measured for the matrix model
- Observation - Additional observations recorded by database compilers
- MatrixDimension - Dimension of the **A** matrix
- SurvivalIssue - Denotes the maximum stage-specific survival value

Slot **version** - A list with the following elements:

- Version - The version number of the database
- DateCreated - The date that the .RData file was created
- Agreement - Link to the COMADRE license agreement

An object of class CompadreDB with 150 rows and 48 columns.

An object of class CompadreDB with 150 rows and 48 columns.

CompadreDB

CompadreDB Class

Description

This page describes the CompadreDB class, including methods for accessing the slots (see functions CompadreData and VersionData), accessing (\$) and replacing (\$<-) columns within the data slot, accessing elements from the version slot (see functions VersionData and DateCreated), and converting legacy database objects to the CompadreDB class (see as_cdb).

Usage

```

CompadreData(object)

## S4 method for signature 'CompadreDB'
CompadreData(object)

## S4 method for signature 'CompadreDB'
x$name

## S4 replacement method for signature 'CompadreDB'
x$name <- value

## S4 method for signature 'CompadreDB,ANY,missing'
x[[i, j, ...]]

## S4 replacement method for signature 'CompadreDB,ANY,missing'
x[[i, j]] <- value

VersionData(object)

## S4 method for signature 'CompadreDB'
VersionData(object)

Version(object)

## S4 method for signature 'CompadreDB'
Version(object)

DateCreated(object)

## S4 method for signature 'CompadreDB'
DateCreated(object)

```

Arguments

object	A CompadreDB object
x	A CompadreDB object
name	The name of a column within x
value	Vector of values to assign to the column
i, j	elements to extract or replace (see [.data.frame])
...	ignored

Slots

data A tibble-style data frame with a list-column of matrix population models (column `mat`) and a variety of other metadata columns.

version A list with elements Version (database version number), DateCreated (date of version release), and Agreement (a url link to the User Agreement)

Author(s)

Iain M. Stott

Tamora D. James

See Also

[CompadreDB-Methods](#) [CompadreDB-Subsetting](#)

Examples

```
# extract entire 'data' slot
dat <- CompadreData(Compadre)

# access the date of database creation
DateCreated(Compadre)

# extract column SpeciesAccepted
Compadre$SpeciesAccepted

# create new list-column with stage-specific survival
Compadre$stage_survival <- lapply(Compadre$mat, function(x) colSums(x@matU))
```

CompadreDB-Methods *Methods for CompadreDB objects*

Description

This page describes a variety of methods that can be used with CompadreDB objects, including common data frame operations (head, names, and merge), conversion methods (as.data.frame and as_tibble), and methods to calculate the number of species (NumberAcceptedSpecies), studies (NumberStudies), or matrices (NumberMatrices).

Usage

```
## S3 method for class 'CompadreDB'
as.data.frame(x, ...)

## S3 method for class 'CompadreDB'
as_tibble(x)

## S3 method for class 'CompadreDB'
head(x, n = 6L, ...)
```

```

## S3 method for class 'CompadreDB'
tail(x, n = 6L, ...)

## S3 method for class 'CompadreDB'
names(x)

## S3 method for class 'CompadreDB'
dim(x)

## S3 method for class 'CompadreDB'
merge(x, y, ...)

NumberAcceptedSpecies(object)

## S4 method for signature 'CompadreDB'
NumberAcceptedSpecies(object)

NumberStudies(object)

## S4 method for signature 'CompadreDB'
NumberStudies(object)

NumberMatrices(object)

## S4 method for signature 'CompadreDB'
NumberMatrices(object)

```

Arguments

x, object	A CompadreDB object
...	additional arguments
n	The number of rows to extract
y	A data.frame to merge with x

Value

No return value, called for side effects

CompadreDB-Subsetting *Subsetting CompadreDB objects*

Description

CompadreDB objects can be subset just like a regular `data.frame`, using either `[]` or `subset()`. Note, however, that the `mat` column will always be retained during subsetting, even if it is not included in the user's column subset.

Usage

```
## S4 method for signature 'CompadreDB,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S3 method for class 'CompadreDB'
subset(x, subset, select, drop = FALSE, ...)
```

Arguments

x	A CompadreDB object
i	row indices (see [.data.frame])
j	column indices (see [.data.frame])
...	ignored
drop	ignored
subset	logical expression indicating which rows to keep
select	expression indicating which columns to keep

Value

No return value, called for side effects

Examples

```
# subset to the first 10 rows
Compadre[1:10,]

# subset to the species 'Echinacea angustifolia'
subset(Compadre, SpeciesAccepted == "Echinacea angustifolia")

# remove the column SurvivalIssue
Compadre[,names(Compadre) != "SurvivalIssue"]

## Not run:
# column selection doesn't include mat, but mat will still be returned with a
# along with a warning
subset(Compadre, select = c("SpeciesAccepted", "Authors"))

## End(Not run)
```

CompadreDB-Tidyverse *Tidyverse methods for CompadreDB objects*

Description

CompadreDB methods for functions in [dplyr](#) and [ggplot2](#).

Usage

```
fortify.CompadreDB(model, data, ...)  
  
filter.CompadreDB(.data, ...)  
  
slice.CompadreDB(.data, ...)  
  
arrange.CompadreDB(.data, ...)  
  
mutate.CompadreDB(.data, ...)  
  
group_by.CompadreDB(.data, ..., add = FALSE)  
  
ungroup.CompadreDB(x, ...)  
  
summarize.CompadreDB(.data, ...)  
  
summarise.CompadreDB(.data, ...)  
  
select.CompadreDB(.data, ...)  
  
rename.CompadreDB(.data, ...)  
  
left_join.CompadreDB(  
  x,  
  y,  
  by = NULL,  
  copy = FALSE,  
  suffix = c(".x", ".y"),  
  ...  
)  
  
right_join.CompadreDB(  
  x,  
  y,  
  by = NULL,  
  copy = FALSE,  
  suffix = c(".x", ".y"),  
  ...  
)  
  
inner_join.CompadreDB(  
  x,  
  y,  
  by = NULL,  
  copy = FALSE,  
  suffix = c(".x", ".y"),  
  ...  
)
```

```

)

full_join.CompadreDB(
  x,
  y,
  by = NULL,
  copy = FALSE,
  suffix = c(".x", ".y"),
  ...
)

```

Arguments

data	see fortify
...	other arguments
add	Logical indicating whether to overwrite existing groups (FALSE) or add to any existing groups (TRUE)
x, model, .data	A CompadreDB object
y	see join
by	see join
copy	see join
suffix	see join

Value

No return value, called for side effects

CompadreLegacy	<i>Subsample of a legacy version of the COMPADRE Plant Matrix Database for testing and examples</i>
----------------	---

Description

CompadreLegacy is a subsample of the COMPADRE Plant Matrix Database in the legacy format (class 'list'), for use in testing and examples. For full documentation see the [COMPADRE User Guide](#).

Usage

```
CompadreLegacy
```

Format

A list with four elements:

metadata - A data frame with the following 47 columns:

- SpeciesAuthor - Binomial species name given by the paper's author
- SpeciesAccepted - Accepted binomial species name taken from *The Plant List* or *Catalogue of Life*
- CommonName - Common name for species used in the publication
- Genus - Taxonomic genus that the accepted species belongs to
- Family - Family that the species belongs to
- Order - Order that the species belongs to
- Class - Class that the species belongs to
- Phylum - Phylum that the species belongs to
- Kingdom - Kingdom that the species belongs to
- OrganismType - Organism type (see COMPADRE User Guide for documentation)
- DicotMonoc - Whether the species is a dicot or monocot. Non-angiosperms are NA.
- AngioGymno - Whether the species is an angiosperm or gymnosperm. Non-plants are NA.
- Authors - Last name of all authors (separated with ";")
- Journal - Abbreviated journal title, or type of source document (e.g. "PhD thesis")
- YearPublication - Year of publication
- DOI.ISBN - Digital Object Identifier or International Standard Book Number codes to identify each publication
- AdditionalSource - Additional source(s) used to reconstruct the matrix or obtain additional metadata for the matrix (if applicable)
- StudyDuration - Number of years of observation in study (StudyEnd - StudyStart)
- StudyStart - Study start year
- StudyEnd - Study end year
- AnnualPeriodicity - Inverse of the length of the projection interval (in years)
- NumberPopulations - The number of study populations as defined by the authors. Within site replication of permanent plots is not defined as separate populations
- MatrixCriteriaSize - Indicates whether the matrix contains stages based on size. If so, indicates what that measure of size is
- MatrixCriteriaOntogeny - Indicates whether the matrix contains stages based on ontogenic/developmental stages
- MatrixCriteriaAge - Indicates whether the matrix contains stages based on age
- MatrixPopulation - Population name or definition of where the matrix was recorded, usually given by the author. See COMPADRE User Guide.
- Lat - Latitude in decimal degrees
- Lon - Longitude in decimal degrees

- Altitude - Altitude of study site (m above sea level)
- Country - 3-letter ISO country code for the country in which the study took place (multiple countries separated with ";")
- Continent - Continent on which study took place
- Ecoregion - Ecoregion in which study took place. See COMPADRE User Guide.
- StudiedSex - Whether study included only males ("M"), only females ("F"), or both sexes ("M/F")
- MatrixComposite - Indicates the type of matrix population model. Possible values are Individual, Mean, Pooled, and Seasonal. See COMPADRE User Guide.
- MatrixTreatment - Describes if a treatment was applied to the population or not. If yes, includes a brief description of the treatment. If not, Unmanipulated
- MatrixCaptive - Whether species was studied in the wild (W), captivity (C), or captured from a wild population (CW)
- MatrixStartYear - First year of matrix
- MatrixStartSeason - First season of matrix as described by author (hemisphere-specific)
- MatrixStartMonth - First month of matrix
- MatrixEndYear - Final year of matrix
- MatrixEndSeason - Final season of matrix as described by author (hemisphere-specific)
- MatrixEndMonth - Final month of matrix
- MatrixSplit - Whether the **A** matrix has been split into components **U**, **F**, and **C** ("Divided") or not ("Indivisible"). If not, elements of `matU`, `matF`, and `matC` are filled with NA
- MatrixFec - Whether fecundity was measured for the matrix model
- Observation - Additional observations recorded by database compilers
- MatrixDimension - Dimension of the **A** matrix
- SurvivalIssue - Denotes the maximum stage-specific survival value

mat - A list of population projection models, which are also in list format. Each list element contains four matrices:

- `matA` - A matrix population model
- `matU` - The survival- and growth-related component of `matA`
- `matF` - The sexual reproduction component of `matA`
- `matC` - The clonal reproduction component of `matA`

matrixClass - A list of data frames, each with the following columns:

- `MatrixClassOrganized` - Standardized stage class of the matrix population model
- `MatrixClassAuthor` - Stage description from the original publication
- `MatrixClassNumber` - Integer stage number

version - A list with the following elements:

- `Version` - The version number of the database

- DateCreated - The date that the .RData file was created
- NumberAcceptedSpecies - The number of accepted species in the original version
- NumberStudies - The number of studies in the original version
- NumberMatrices - The number of matrices in the original version
- Agreement - Link to the COMADRE license agreement

CompadreMatrixMethods *Methods for working with matrices in com(p)adre*

Description

This page describes methods for accessing any matrix information from CompadreMat and CompadreDB objects.

Most methods for working with matrices are applicable to both CompadreMat and CompadreDB objects. These are described on this page (along with a couple) of methods applicable to only CompadreMat or CompadreDB objects).

Usage

```
matA(object)

## S4 method for signature 'CompadreMat'
matA(object)

## S4 method for signature 'CompadreDB'
matA(object)

## S4 method for signature 'list'
matA(object)

matU(object)

## S4 method for signature 'CompadreMat'
matU(object)

## S4 method for signature 'CompadreDB'
matU(object)

## S4 method for signature 'list'
matU(object)

matF(object)

## S4 method for signature 'CompadreMat'
matF(object)
```

```
## S4 method for signature 'CompadreDB'  
matF(object)  
  
## S4 method for signature 'list'  
matF(object)  
  
matC(object)  
  
## S4 method for signature 'CompadreMat'  
matC(object)  
  
## S4 method for signature 'CompadreDB'  
matC(object)  
  
## S4 method for signature 'list'  
matC(object)  
  
matrixClass(object)  
  
## S4 method for signature 'CompadreMat'  
matrixClass(object)  
  
## S4 method for signature 'CompadreDB'  
matrixClass(object)  
  
## S4 method for signature 'list'  
matrixClass(object)  
  
MatrixClassAuthor(object)  
  
## S4 method for signature 'CompadreMat'  
MatrixClassAuthor(object)  
  
## S4 method for signature 'CompadreDB'  
MatrixClassAuthor(object)  
  
## S4 method for signature 'list'  
MatrixClassAuthor(object)  
  
MatrixClassOrganized(object)  
  
## S4 method for signature 'CompadreMat'  
MatrixClassOrganized(object)  
  
## S4 method for signature 'CompadreDB'  
MatrixClassOrganized(object)
```

```

## S4 method for signature 'list'
MatrixClassOrganized(object)

MatrixClassNumber(object)

## S4 method for signature 'CompadreMat'
MatrixClassNumber(object)

## S4 method for signature 'CompadreDB'
MatrixClassNumber(object)

## S4 method for signature 'list'
MatrixClassNumber(object)

```

Arguments

object A CompadreDB object

Slots

matA A matrix population model (i.e. a square projection matrix)

matU The survival component of a matrix population model (i.e. a square projection matrix reflecting survival-related transitions; e.g. progression, stasis, and retrogression)

matF The sexual component of a matrix population model (i.e. a square projection matrix reflecting transitions due to sexual reproduction)

matC The clonal component of a matrix population model (i.e. a square projection matrix reflecting transitions due to clonal reproduction)

matrixClass A data frame with columns MatrixClassOrganized (elements are "active", "prop", or "dorm") MatrixClassAuthor (the matrix author's stage description), and MatrixClassNumber (integer stage number)

mpm_mean

Calculate a mean over a list of matrices or CompadreMat objects

Description

Calculates an element-wise mean over a list of matrices or CompadreMat objects of constant dimension.

Usage

```
mat_mean(x, na.rm = FALSE)
```

```
mpm_mean(x, na.rm = FALSE)
```

Arguments

x	List of matrices (mat_mean) or list of CompadreMat objects (mpm_mean), all of same dimension
na.rm	Logical indicating whether missing values should be excluded (see <i>Details</i>). Defaults to FALSE.

Details

If na.rm == TRUE, missing values are ignored in the calculation of the mean matrix. If na.rm == TRUE and a given element is NA in *every* matrix within x, the value returned for that element will be \emptyset .

Value

A matrix (mat_mean) or a CompadreMat object (mpm_mean).

Author(s)

Patrick Barks <patrick.barks@gmail.com>

Owen R. Jones <jones@biology.sdu.dk>

See Also

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [string_representation](#)

Examples

```
# there are four rows for species 'Haplopappus_radiatus' in Compadre
mpms <- Compadre$mat[Compadre$SpeciesAuthor == "Haplopappus_radiatus"]
mpm_mean(mpms)

# extract list of matA and take mean
mats <- matA(mpms)
mat_mean(mats)
```

mpm_methods

Extract stage-class information from CompadreMat or CompadreDB objects

Description

Methods for extracting stage-class information from CompadreMat or CompadreDB objects, including whether the matrix population model includes one or more propagule stages (mpm_has_prop), dormant stages (mpm_has_dorm), or active stages (mpm_has_active), and the integer index of the first active stage class (mpm_first_active).

These methods will return a single value if passed a CompadreMat object, or a vector of values if passed a CompadreDB object (one value for every CompadreMat object within the column 'mat').

Usage

```
mpm_has_prop(object)

## S4 method for signature 'CompadreMat'
mpm_has_prop(object)

## S4 method for signature 'CompadreDB'
mpm_has_prop(object)

mpm_has_active(object)

## S4 method for signature 'CompadreMat'
mpm_has_active(object)

## S4 method for signature 'CompadreDB'
mpm_has_active(object)

mpm_has_dorm(object)

## S4 method for signature 'CompadreMat'
mpm_has_dorm(object)

## S4 method for signature 'CompadreDB'
mpm_has_dorm(object)

mpm_first_active(object)

## S4 method for signature 'CompadreMat'
mpm_first_active(object)

## S4 method for signature 'CompadreDB'
mpm_first_active(object)
```

Arguments

object A CompadreMat or CompadreDB object

Value

No return value, called for side effects

Author(s)

Patrick Barks <patrick.barks@gmail.com>

See Also

Other data checking: [cdb_check_species\(\)](#), [cdb_collapse\(\)](#), [cdb_compare\(\)](#), [cdb_flag\(\)](#)

Examples

```
# with CompadreMat object
mpm_has_prop(Compadre$mat[[1]])
mpm_has_active(Compadre$mat[[1]])
mpm_has_dorm(Compadre$mat[[1]])
mpm_first_active(Compadre$mat[[1]])
```

```
# with CompadreDB object
mpm_has_prop(Compadre)
mpm_has_active(Compadre)
mpm_has_dorm(Compadre)
mpm_first_active(Compadre)
```

string_representation *Convert vectors or square numeric matrices to and from string representation*

Description

Functions to convert vectors or square numeric matrices to and from string representation, which is primarily useful for writing data frames with list-columns containing vectors or matrices to a flat file format such as csv.

String representations of vectors and matrices begin with an open bracket "[" and end with a closed bracket "]". Matrix elements are separated with a space ("[0.2 0.3 0.1 0]") whereas vector elements are separate with two vertical bars ("[Seedling||Juvenile||Reproductive]").

Usage

```
mat_to_string(mat)

vec_to_string(vec)

string_to_mat(mat_str)

string_to_vec(vec_str, numeric = FALSE)
```

Arguments

mat	A square numeric matrix
vec	A vector
mat_str	A square numeric matrix in string representation
vec_str	A vector in string representation
numeric	Logical value indicating whether a string representation of a vector should be coerced to numeric (if FALSE remains character)

Value

A square numeric matrix (`string_to_mat`), vector (`string_to_vec`), or string (`mat_to_string` or `vec_to_string`).

Author(s)

Owen R. Jones <jones@biology.sdu.dk>

Patrick M. Barks <patrick.barks@gmail.com>

See Also

[cdb_flatten](#) [cdb_unflatten](#)

Other data management: [cdb_flatten\(\)](#), [cdb_id_stages\(\)](#), [cdb_id_studies\(\)](#), [cdb_id\(\)](#), [cdb_mean_matF\(\)](#), [cdb_rbind\(\)](#), [cdb_unflatten\(\)](#), [cdb_unnest\(\)](#), [mpm_mean\(\)](#)

Examples

```
mat_str <- "[3.3 5.2 6.1 0.1 NA 0.3 0.2 0.4 0.1]"
mat <- string_to_mat(mat_str)

vec1_str <- "[0.30||0.42||0.19||0.09]"
vec1 <- string_to_vec(vec1_str, numeric = TRUE)

vec2_str <- "[Seedling 1||Seedling 2||Juvenile||Reproductive]"
vec2 <- string_to_vec(vec2_str)

# convert back to string format
mat_to_string(mat)
vec_to_string(vec1)
vec_to_string(vec2)

## Not run:
# non-square matrix
mat_str <- "[0.42 0.52 0.15 0.23 0.14]"
string_to_mat(mat_str)

## End(Not run)
```

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