Package ‘EML’

February 8, 2020

Type Package
Title Read and Write Ecological Metadata Language Files
Description Work with Ecological Metadata Language (‘EML’) files. 
‘EML’ is a widely used metadata standard in the ecological and 
environmental sciences, described in Jones et al. (2006), 

Version 2.0.2
License MIT + file LICENSE
BugReports https://github.com/ropensci/EML/issues
Encoding UTF-8
LazyData true
Depends R (>= 2.10)
Suggests knitr, taxadb, tibble, testthat, covr, EML, units,
htmlwidgets, shiny, shinyjs, spelling
Imports xml2, methods, digest, emld (>= 0.4.0), jqr, jsonlite, uuid,
markdown, utils, dplyr
VignetteBuilder knitr
RoxygenNote 7.0.2
Language en-US
Additional_repositories https://cboettig.github.io/drat
NeedsCompilation no
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**Description**

builds factor table for shiny app

**Usage**

build_factors(att_table, data)
**Build Units Table**

**Arguments**
- `att_table` (data.frame) input attributes table
- `data` (data.frame) input data

**Description**
Builds unit table for shiny app.

**Usage**
```r
build_units_table(in_units, eml_units)
```

**Arguments**
- `in_units` input units
- `eml_units` eml units

**Detect Delim**

**Description**
This helper function was written expressly for `set_physical` to be able to automate its `recordDelimiter` argument.

**Usage**
```r
detect_delim(path, nchar = 1000)
```

**Arguments**
- `path` (character) File to search for a delimiter
- `nchar` (numeric) Maximum number of characters to read from disk when searching

**Value**
(character) If found, the delimiter, it not, `\n`
Description

eml_get

Format

A list with constructor functions

Usage

eml_get(x, element, from = "list", ...)

Arguments

x

an EML object or child/descendant object

element

name of the element to be extracted. If multiple occurrences are found, will extract all

from

explicit type for the input format. Possible values: "xml", "json", "list", or "guess" with "list" as the default.

...

additional arguments

Examples

f <- system.file("tests", emld::eml_version(), "eml-datasetWithUnits.xml", package = "emld")
eml <- read_eml(f)
eml_get(eml, "physical")
eml_get(eml, "attributeList")

## The first argument need not be an "eml" class, it could be a child element; e.g.
eml_get(eml$dataset$dataTable, "physical")
## Description

eml_validate processes an EML document using the XSD schema for the appropriate version of EML and determines if the document is schema-valid as defined by the XSD specification.

## Usage

```r
eml_validate(eml, encoding = "UTF-8", schema = NULL)
```

## Arguments

- **eml**: file path, xml_document,
- **encoding**: optional encoding for files, default UTF-8.
- **schema**: path to schema

## Value

Whether the document is valid (logical)

## Note

This function is simply an alias to `eml_validate` in `emld` package.

## Examples

```r
f <- system.file("extdata", "example.xml", package = "emld")

## validate file directly from disk:
eml_validate(f)

## validate an eml object:
eml <- read_eml(f)
eml_validate(eml)
```
Description

get_attributes

Usage

get_attributes(x, eml = NULL)

Arguments

x
  an "attributeList" element from an emld object
eml
  The full eml document, needed only if <references> outside of attributes must be resolved.

Details

EML metadata can use "references" elements which allow one attribute to use metadata declared elsewhere in the document. This function will automatically resolve these references and thus infer the correct metadata.

Value

A data frame whose rows are the attributes (names of each column in the data file) and whose columns describe metadata about those attributes. By default separate tables are given for each type.

Examples

f <- system.file("tests", emld::eml_version(),
  "eml-datasetWithAttributelevelMethods.xml", package = "emld")
eml <- read_eml(f)
get_attributes(eml$dataset$DataTable$attributeList)

get_numberType

Description

Get EML numberType

returns the EML numberType (either 'real', 'integer', 'whole', or 'natural') of input values

Usage

get_numberType(values)
Arguments

values (numeric/character) a vector of values, if vector is non-numeric will return NA

Value

the numberType of values (either 'real', 'integer', 'whole', or 'natural').

Examples

```r
## Not run:
# To get numberType for each column in a data.frame:
unlist(lapply(df, function(x) get_numberType(x)))
## End(Not run)
```

Description

get_unitList

Usage

get_unitList(x = NULL)

Arguments

x an emld object

Details

If no unitList is provided, the function reads in the eml-unitDictionary defining all standard units and unitTypes. This provides a convenient way to look up standard units and their EML-recognized names when defining metadata, e.g. in the table passed to `set_attributes()`.

Value

a list with two data.frames: "units", a table defining unit names, types, and conversions to SI, and "unitTypes", defining the type of unit. For instance, the unit table could define "Hertz" as a unit of unitType frequency, and the unitType define frequency as a type whose dimension is 1/time.
Examples

# Read in additional units defined in a EML file

f <- system.file("tests", emld::eml_version(),
    "eml-datasetWithUnits.xml",
    package = "emld"
)
eml <- read_eml(f)
unitList <- get_unitList(eml)

## Read in the definitions of standard units:
get_unitList()

describe(get_unit_id)

description

get_unit_id(input_units, eml_version = emld::eml_version())

Arguments

input_units (character|vector) input units that needs valid EML unit ids
eml_version (character) the eml schema version desired (there is a change in the way eml
    units are named from eml-2.1.1 to eml-2.2.0)

Value

(character) A valid EML unit id. If no valid EML unit id can be found, the function will output a
warning, along with a preformatted custom unit id.

Examples

## Not run:
# The following all return the same id
get_unit_id("kilometersPerSquareSecond")
get_unit_id("kilometerPerSecondSquared")
get_unit_id("Kilometers per seconds squared")
get_unit_id("km/s^2")
htmlwidgets_attributes

Description

Used to call handsontable html widget to build attributes

Usage

htmlwidgets_attributes(df, type = NULL)

Arguments

df (data.frame) the data.frame of data that needs an attribute table
type (character) either "attributes", "units", or "factors"

is_standardUnit

Description

is_standardUnit

Usage

is_standardUnit(x)

Arguments

x name of unit to check

Value

TRUE if unit is exact match to the id of a unit in the Standard Units Table, FALSE otherwise.

Examples

is_standardUnit("amperePerMeter") # TRUE
is_standardUnit("speciesPerSquareMeter") # FALSE
### read_eml

**Description**

Read an EML file into R as an emld object.

**Usage**

```r
read_eml(x, from = "xml")
```

**Arguments**

- `x`: path to an EML file
- `from`: explicit type for the input format. Possible values: "xml", "json", "list", or "guess" with "xml" as the default.

**Value**

an emld object (list / S3 object)

**Examples**

```r
f <- system.file("extdata", "example.xml", package = "emld")
eml <- read_eml(f)
```

### set_attributes

**Description**

set_attributes

**Usage**

```r
set_attributes(attributes, factors = NULL, col_classes = NULL, missingValues = NULL)
```

**Examples**

```r
f <- system.file("extdata", "example.xml", package = "emld")
eml <- read_eml(f)
```
Arguments

attributes  a joined table of all attribute metadata
factors  a table with factor code-definition pairs; see details
col_classes  optional, list of R column classes ('ordered', 'numeric', 'factor', 'Date', or 'character', case sensitive) will let the function infer missing 'domain' and 'measurementScale' values for attributes column. Should be in same order as attributeNames in the attributes table, or be a named list with names corresponding to attributeNames in the attributes table.
missingValues  optional, a table with missing value code-definition pairs; see details

Details

The attributes data frame must use only the recognized column headers shown here. The attributes data frame must contain columns for required metadata. These are:

For all data:

• attributeName (required, free text field)
• attributeDefinition (required, free text field)
• measurementScale (required, "nominal", "ordinal", "ratio", "interval", or "dateTime", case sensitive) but it can be inferred from col_classes.
• domain (required, "numericDomain", "textDomain", "enumeratedDomain", or "dateTimeDomain", case sensitive) but it can be inferred from col_classes.

For numeric (ratio or interval) data:

• unit (required). Unitless values should use "dimensionless" as the unit.

For character (textDomain) data:

• definition (required)

For dateTime data:

• formatString (required)

Other optional allowed columns in the attributes table are: source, pattern, precision, numberType, missingValueCode, missingValueCodeExplanation, attributeLabel, storageType, minimum, maximum

The factors data frame, required for attributes in an enumerated domain, must use only the following recognized column headers:

• attributeName (required)
• code (required)
• definition (required)

The missingValues data frame, optional, can be used in the case that multiple missing value codes need to be set for the same attribute. This table must contain the following recognized column headers.
• attributeName (required)
• code (required)
• definition (required)

Value
an eml "attributeList" object

set_coverage
set_coverage

Description
set_coverage

Usage

set_coverage(
  beginDate = character(),
  endDate = character(),
  date = character(),
  sci_names = character(),
  geographicDescription = character(),
  westBoundingCoordinate = numeric(),
  eastBoundingCoordinate = numeric(),
  northBoundingCoordinate = numeric(),
  southBoundingCoordinate = numeric(),
  altitudeMinimum = numeric(),
  altitudeMaximum = numeric(),
  altitudeUnits = character()
)

Arguments

beginDate Starting date for temporal coverage range.
endDate End date for temporal coverage range
date give a single date, or vector of single dates covered (instead of beginDate and
sciname string (space separated) or list or data frame of scientific names for species covered. See details
geographicDescription text string describing the geographic location
westBoundingCoordinate Decimal longitude for west edge bounding box
eastBoundingCoordinate Decimal longitude for east edge bounding box
set_coverage provides a simple and concise way to specify most common temporal, taxonomic, and geographic coverage metadata. For certain studies this will not be well suited, and users will need the more flexible but more verbose construction using "new()" methods; for instance, to specify temporal coverage in geological epoch instead of calendar dates, or to specify taxonomic coverage in terms of other ranks or identifiers.

**Value**

a coverage object for EML

**Note**

If "sci_names" is a data frame, column names of the data frame are rank names. For user-defined "sci_names", users must make sure that the order of rank names they specify is from high to low. Ex. "Kingdom","Phylum","Class","Order","Family","Genus","Species","Common"

**Examples**

```r
coverage <-
  set_coverage(
    begin = "2012-06-01", end = "2013-12-31",
    sci_names = "Sarracenia purpurea",
    geographicDescription = "California coast, down through Baja, Mexico",
    west = -122.44, east = -117.15,
    north = 37.38, south = 30.00
  )
```

---

**Description**

set_methods
Usage

```r
set_methods(
  methods_file,
  instrumentation = character(),
  software = NULL,
  sampling_file = NULL,
  sampling_coverage = NULL,
  sampling_citation = NULL,
  qualityControl_file = NULL
)
```

Arguments

- **methods_file**: Path to a file (markdown or .docx) containing a description of the methods used
- **instrumentation**: optional, text describing instrumentation used in methods
- **software**: optional, an EML software node describing software used in methods
- **sampling_file**: optional, Path to a file (.md or .docx) describing sampling method
- **sampling_coverage**: optional, coverage node for methods, e.g. `set_coverage()`
- **sampling_citation**: optional, a citation element describing the sampling protocol
- **qualityControl_file**: optional, path to a file (.md or .docx) describing quality control methods

Value

A methods object

Examples

```r
f <- system.file("examples/hf205-methods.md", package = "EML")
set_methods(methods_file = f)

## Can also import from methods written in a .docx MS Word file.
f <- system.file("examples/hf205-methods.docx", package = "EML")
set_methods(methods_file = f)
```
Description

Will calculate the file size, checksum, and checksum authentication method algorithm automatically if the argument objectName is a file that exists.

Usage

```r
set_physical(
  objectName,
  id = character(),
  numHeaderLines = character(),
  numFooterLines = character(),
  recordDelimiter = detect_delim(objectName),
  fieldDelimiter = ",",
  collapseDelimiters = logical(),
  literalCharacter = character(),
  quoteCharacter = character(),
  attributeOrientation = "column",
  size = NULL,
  sizeUnit = "bytes",
  authentication = NULL,
  authMethod = NULL,
  characterEncoding = character(),
  encodingMethod = character(),
  compressionMethod = character(),
  url = character()
)
```

Arguments

- **objectName**: name for the object, usually a filename like "hf205-1.csv"
- **id**: optional, an id value for the `<physical>` element in EML, for use in referencing
- **numHeaderLines**: Number of header lines preceding data. Lines are determined by the physicalLineDelimiter, or if it is absent, by the recordDelimiter. This value indicated the number of header lines that should be skipped before starting to parse the data.
- **numFooterLines**: Number of footer lines following data. Lines are determined by the physicalLineDelimiter, or if it is absent, by the recordDelimiter. This value indicated the number of footer lines that should be skipped after parsing the data. If this value is omitted, parsers should assume the data continues to the end of the data stream.
- **recordDelimiter**: This element specifies the record delimiter character when the format is text. The record delimiter is usually a linefeed (`\n`) on UNIX, a carriage return (`\r`) on
MacOS, or both (\r\n) on Windows/DOS. Multiline records are usually delimited with two line ending characters, for example on UNIX it would be two linefeed characters (\n\n). As record delimiters are often non-printing characters, one can use either the special value "\n" to represent a linefeed (ASCII 0x0a) and "\r" to represent a carriage return (ASCII 0x0d). Alternatively, one can use the hex value to represent character values (e.g., 0x0a).

fieldDelimiter "," character by default (for csv files). This element specifies a character to be used in the object for indicating the ending column for an attribute. The delimiter character itself is not part of the attribute value, but rather is present in the column following the last character of the value. Typical delimiter characters include commas, tabs, spaces, and semicolons. The only time the fieldDelimiter character is not interpreted as a delimiter is if it is contained in a quoted string (see quoteCharacter) or is immediately preceded by a literalCharacter. Non-printable quote characters can be provided as their hex values, and for tab characters by its ASCII string "\t". Processors should assume that the field starts in the column following the previous field if the previous field was fixed, or in the column following the delimiter from the previous field if the previous field was delimited.

collapseDelimiters
The collapseDelimiters element specifies whether sequential delimiters should be treated as a single delimiter or multiple delimiters. An example is when a space delimiter is used; often there may be several repeated spaces that should be treated as a single delimiter, but not always. The valid values are yes or no. If it is set to yes, then consecutive delimiters will be collapsed to one. If set to no or absent, then consecutive delimiters will be treated as separate delimiters. Default behavior is no; hence, consecutive delimiters will be treated as separate delimiters, by default.

literalCharacter
This element specifies a character to be used for escaping special character values so that they are treated as literal values. This allows "escaping" for special characters like quotes, commas, and spaces when they are intended to be used in an attribute value rather than being intended as a delimiter. The literalCharacter is typically a \.

quoteCharacter
This element specifies a character to be used in the object for quoting values so that field delimiters can be used within the value. This basically allows delimiter "escaping". The quoteCharacter is typically a ‘ ‘or ’’. When a processor encounters a quote character, it should not interpret any following characters as a delimiter until a matching quote character has been encountered (i.e., quotes come in pairs). It is an error to not provide a closing quote before the record ends. Non-printable quote characters can be provided as their hex values.

attributeOrientation
Specifies whether the attributes described in the physical stream are found in columns or rows. The valid values are column or row. If set to 'column', then the attributes are in columns. If set to 'row', then the attributes are in rows. Row orientation is rare.

size
This element contains information of the physical size of the entity, by default represented in bytes unless the sizeUnit attribute is provided to change the units.
set_responsibleParty

sizeUnit  the unit in which size is measured; default is 'bytes'

authentication  This element describes authentication procedures or techniques, typically by giving a checksum value for the object. The method used to compute the authentication value (e.g., MD5) is listed in the method attribute.

authMethod  the method for authentication checksum, e.g. MD5

characterEncoding  This element contains the name of the character encoding. This is typically ASCII or UTF-8, or one of the other common encodings.

encodingMethod  This element lists a encoding method used to encode the object, such as base64, BinHex.

compressionMethod  This element lists a compression method used to compress the object, such as zip, compress, etc. Compression and encoding methods must be listed in the order in which they were applied, so that decompression and decoding should occur in the reverse order of the listing. For example, if a file is compressed using zip and then encoded using MIME base64, the compression method would be listed first and the encoding method second.

url  optional. The complete url from which the data file can be downloaded, if possible.

Value
an EML physical object, such as used in a dataTable element to define the format of the data file.

Examples

set_physical("hf205-01-TPexp1.csv")
# FIXME set recordDelimiter based on user's system?
# FIXME richer distribution options? use set_distribution at top level?

Description

set_responsibleParty

Usage

set_responsibleParty(
  givenName = NULL,
  surName = NULL,
  organizationName = NULL,
  positionName = NULL,
  address = NULL,
  phone = NULL,
set_software

electronicMailAddress = NULL,
onlineUrl = NULL,
userId = NULL,
id = NULL,
email = NULL
)

Arguments

givenName individual’s given names (list or vector for multiple names). OR a person object.
surName individual name
organizationName if party is an organization instead of an individual, name for the org
positionName individual’s position, i.e. "Researcher", "Graduate Student", "Professor"
address address object, see ‘emlAddress’ to build an address object
phone individual or organization phone number
electronicMailAddress email address (alternatively, can use ‘email’ argument)
onlineUrl a URL to the homepage of the individual or organization
userId the user’s ID, usually within a particular system (KNB, DataONE)
id Identifier for this block, ideally an ORCID id (optional)
email alias for electronicMailAddress

Value

A emld object for any responsibleParty (e.g. creator, contact, etc)

Examples

carl <- set_responsibleParty(as.person("Carl Boettiger <cboettig@ropensci.org>"))
matt <- set_responsibleParty("Matthew", "Jones", email = "mbjones@nceas.ucsb.edu")

Description

set_software

Usage

set_software(codemeta)

Arguments

codemeta codemeta object, see examples
set_taxonomicCoverage

**Value**

an eml software element

**Examples**

cm <- jsonlite::read_json(system.file("extdata/codemeta.json", package = "EML"))
software <- set_software(cm)
my_eml <- eml$eml(packageId = "eml-1.2", system = "knb", software = software)

# write_eml(my_eml, "test.xml")

---

**set_taxonomicCoverage**

**set_taxonomicCoverage**

**Description**

set_taxonomicCoverage

**Usage**

set_taxonomicCoverage(sci_names, expand = FALSE, db = "itis")

**Arguments**

- **sci_names**
  - string (space separated) or list or data frame of scientific names for species covered.
- **expand**
  - Set to TRUE to use `[taxadb]` to expand sci_names into full taxonomic classifications
- **db**
  - The taxonomic database to query (when expand is set to TRUE). See `[taxadb::filter_name]` for valid options. Defaults to `itis`.

**Details**

Turn a data.frame or a list of scientific names into a taxonomicCoverage block sci_names can be a space-separated character string or a data frame with column names as rank name or a list of user-defined taxonomicClassification

**Value**

a taxonomicCoverage object for EML

**Note**

If "sci_names" is a data frame, column names of the data frame are rank names. For user-defined "sci_names", users must make sure that the order of rank names they specify is from high to low. Ex. "Kingdom", "Phylum", "Class", "Order", "Family", "Genus", "Species", "Common" EML permits any rank names provided they go in descending order.
Examples

```r
sci_names <- data.frame(
  Kingdom = "Plantae",
  Phylum = "Phaeophyta",
  Class = "Phaeophyceae",
  Order = "Laminariales",
  Family = "Lessoniaceae",
  Genus = "Macrocystis",
  Species = "pyrifera"
)
taxon_coverage <- set_taxonomicCoverage(sci_names)

# Examples that may take > 5s

# Query ITIS using taxadb to fill in the full taxonomy given just species names
taxon_coverage <- set_taxonomicCoverage(
  c("Macrocystis pyrifera", "Homo sapiens"),
  expand = TRUE
)

# Query GBIF instead of ITIS
taxon_coverage <- set_taxonomicCoverage(
  c("Macrocystis pyrifera"),
  expand = TRUE,
  db = "gbif"
)

### use a list of lists for multiple species
sci_names <- list(list(
  Kindom = "Plantae",
  Phylum = "Phaeophyta",
  Class = "Phaeophyceae",
  Order = "Laminariales",
  Family = "Lessoniaceae",
  Genus = "Macrocystis",
  Species = "pyrifera"
))
set_taxonomicCoverage(sci_names)
```

**Description**

For any EML element of class TextType, this function can be used to generate the appropriate EML from a markdown-formatted file.
set_TextType

Usage

set_TextType(file = NULL, text = NULL)

Arguments

file path to a file providing formatted input text, see details.
text a plain text character string which will be used directly as the content of the node
if no file is given

Details

If the 'rmarkdown' package is installed, then the input file can be a Microsoft Word (.docx) file, a markdown file, or other file recognized by Pandoc (see http://pandoc.org), which will automate the conversion to a docbook. Otherwise, the input file should already be in docbook format (with .xml or .dbk extension). Note that pandoc comes pre-installed in RStudio and is required for the rmarkdown package.

Value

a TextType object that can be coerced into any element inheriting from TextType, see examples

Examples

```r
## using a simple character string
a <- set_TextType(text = "This is the abstract")
as(a, "abstract")

## Using an external markdown file
f <- system.file("examples/hf205-abstract.md", package = "EML")
a <- set_TextType(f)
as(a, "abstract")

## Can also import from methods written in a .docx MS Word file.
f <- system.file("examples/hf205-abstract.docx", package = "EML")
a <- set_TextType(f)
as(a, "abstract")

## Documents with title headings use `section` instead of `para` notation
f <- system.file("examples/hf205-methods.docx", package = "EML")
d <- set_TextType(f)
as(d, "description")
```
Description

Define custom units, including new unitTypes. Note that it is not necessary to define most common units.

Usage

set_unitList(units, unitTypes = NULL, as_metadata = FALSE)

Arguments

units a data.frame describing the custom units, see details.
unitTypes optional, a data.frame defining any additional unitTypes not already defined
as_metadata logical, default FALSE. If true, returns an ‘additionalMetadata’ element, see below.

Details

The units data.frame must have the following columns: - id: the referenced name of unit (singular). e.g. ‘meter’, ‘second’ - unitType: the base type of unit, e.g. ‘length’. If not from a standard type, a new unitType must be provided - multiplierToSI: the multiplicative constant to convert to the SI unit. - parentSI: the name of the parent SI unit, e.g. second. - description: a text string describing the unit of measure. The following columns are optional: - name: usually the same as the id of the unit, e.g. second - abbreviation: common abbreviation, e.g. s - constantToSI: an additive constant to convert to the equivalent SI unit. If not given, default is "0"

In practice, researchers may save these tables of custom units they frequently use in an external .csv or other format and read them in to R for ready re-use.

The unitType table must have the following columns: - id: the name by which the unitType is referred to. - name: optional, default is same as the id - dimension: name of a base dimension of the unit - power: the power to which the dimension is raised (NA implies power of 1)

Value

unitList list object

Examples

```r
## create the "unitType" table for custom unit
id <- c("speed", "speed", "acceleration", "acceleration", "frequency")
dimension <- c("length", "time", "length", "time", "time")
power <- c(NA, "-1", NA, "-2", "-1")
unitTypes <- data.frame(
  id = id, dimension = dimension,
  power = power, stringsAsFactors = FALSE
)```

```r
## create the "units" table for custom unit
units <- data.frame(
  id = c("meter", "second", "foot", "foot", "foot"),
  unitType = c("length", "time", "length", "time", "time"),
  multiplierToSI = c(1, 1, 0.3048, 0.3048, 0.3048),
  parentSI = c("meter", "second", "foot", "foot", "foot"),
  description = c("meter", "second", "foot", "foot", "foot"),
  stringsAsFactors = FALSE
)
```
Create the units table

```r
id <- c("minute", "centimeter")
unitType <- c("time", "length")
parentSI <- c("second", "meter")
multiplierToSI <- c("0.0166", "1")
description <- c("one minute is 60 seconds", "centimeter is a 100th of a meter")
units <- data.frame(
  id = id, unitType = unitType, parentSI = parentSI,
  multiplierToSI = multiplierToSI, description = description,
  stringsAsFactors = FALSE
)
```

```r
unitList <- set_unitList(units, unitTypes)
```

---

### shiny_attributes

Create/Edit EML attributes

**Description**

Create/edit EML attributes, custom units, and factors in a shiny environment.

**Usage**

```r
shiny_attributes(data = NULL, attributes = NULL)
```

**Arguments**

- **data** (data.frame) the data.frame of data that needs an attribute table
- **attributes** (data.frame) an existing attributes table

**Details**

Attributes can be created from scratch using `shiny_attributes()`. Or an existing attribute table can be edited using `shiny_attributes(NULL, attributes)`. Or new attributes can be created from a data table using `shiny_attributes(data, NULL)`. If attributes are created from a data table, fields such as 'attributeName' and 'numberType' will be automatically completed based on the attributes within the data table. If both existing attributes and data table are entered (i.e. `shiny_attributes(data, attributes)`), any automatically generated fields based attributes within the data table **will not** override any non-empty fields in the entered attributes.

**Examples**

```r
## Not run:
# from scratch
out <- shiny_attributes(NULL, NULL)

# from data
```
```r
data <- iris
out <- shiny_attributes(data, NULL)

# from existing attributes
file <- system.file("tests", emld::eml_version(),
  "eml-datasetWithAttributeLevelMethods.xml",
  package = "emld"
)
eml <- read_eml(file)
x <- eml$dataset$dataTable$attributeList
df <- get_attributes(x, eml)
out <- shiny_attributes(NULL, df$attributes)

# from attributes and data
out <- shiny_attributes(data, df$attributes)

## End(Not run)
```

### table_to_r

**Description**

Takes a handsontable and converts to r data.frame for shiny app

**Usage**

`table_to_r(table)`

**Arguments**

- `table` input table

### write_eml

**Description**

`write_eml`

**Usage**

`write_eml(eml, file, namespaces = NULL, ns = "eml", ...)`
Arguments

- **eml**: an emld class object
- **file**: file name to write XML.
- **namespaces**: named character vector of additional XML namespaces to use.
- **ns**: root namespace abbreviation
- **...**: additional arguments to `write_xml`

Value

If file is not specified, the result is a character string containing the resulting XML content. Otherwise return silently.

Examples

```r
f <- system.file("extdata", "example.xml", package = "emld")
eml <- read_eml(f)
write_eml(eml, "test.xml")
eml_validate("test.xml")
unlink("test.xml") # clean up
```
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