Package: dbparser (via r-universe)

July 18, 2024

Title Drugs Databases Parser

Version 2.0.3

Description This tool is for parsing public drug databases such as
'DrugBank' XML database <https://go.drugbank.com/>. The parsed
data are then returned in a proper 'R' object called
'dvobject'.

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Encoding UTF-8

Imports dplyr, progress, purrr, tibble, tools, XML

RoxygenNote 7.2.3

Suggests canvasXpress, knitr, rmarkdown, testthat, tidyr

VignetteBuilder knitr

URL https://docs.ropensci.org/dbparser/,
https://github.com/ropensci/dbparser

BugReports https://github.com/ropensci/dbparser/issues

Depends R (>= 3.5)

Repository https://ropensci.r-universe.dev

RemoteUrl https://github.com/ropensci/dbparser

RemoteRef master

RemoteSha 39d9a078503c734a74d5f0fdc693db117e94b40f

Contents

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cett_nodes_options   *returns carriers, enzymes,targets and transporters node valid options.*

Description

returns carriers, enzymes,targets and transporters node valid options.

Usage

```
cett_nodes_options()
```

Value

list of CETT valid options

See Also

Other parsers: `drug_node_options()`, `parseDrugBank()`, `references_node_options()`

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drug_node_options   *returns drug node valid options.*

Description

returns drug node valid options.

Usage

```
drug_node_options()
```

Value

list of drug valid options

See Also

Other parsers: `cett_nodes_options()`, `parseDrugBank()`, `references_node_options()`

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parseDrugBank *parseDrugBank*

Description

parses given DrugBank XML database into a dvobject. dvobject is a list of data.frames in which each data.frame represents a part of parsed data (i.e drugs, prices, carriers, ...)

Usage

```
parseDrugBank(
  db_path,
  drug_options = NULL,
  parse_salts = FALSE,
  parse_products = FALSE,
  references_options = NULL,
  cett_options = NULL
)
```

Arguments

db_path **string**, full path for the **DrugBank** xml or zip file.

drug_options **character vector**, list of sub drug related nodes names options to parse (default = NULL). Check drug_node_options() for all available options. If its value is 'NULL' ONLY 'drug_general_information' will be placed in the returned dvobject.

parse_salts **boolean**, parse salts info (default = FALSE)

parse_products **boolean**, parse products info (default = FALSE)

references_options

character vector, list of sub references related nodes names options to parse (default = NULL). Check references_node_options() for all available options.

cett_options **character vector**, list of sub cett related nodes names options to parse (default = NULL). Check cett_nodes_options() for all available options.

Value

dvobject

See Also

Other parsers: cett_nodes_options(), drug_node_options(), references_node_options()

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references_node_options

returns references node valid options.

Description

returns references node valid options.

Usage

```
references_node_options()
```

Value

list of references valid options

See Also

Other parsers: cett_nodes_options(), drug_node_options(), parseDrugBank()

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show_dvobject_metadata

init_dvobject Returns data.frame with two columns (key, value) of dvobject attributes

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Description

init_dvobject Returns data.frame with two columns (key, value) of dvobject attributes

Usage

```
show_dvobject_metadata(dvobject)
```

Arguments

dvobject   - dvobject list to show related metadata

Value

data.frame

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