Package 'dbparser'

April 20, 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)

NeedsCompilation no

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Repository CRAN

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R topics documented:

| 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](#)()

| 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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