Package: dbparser (via r-universe)

October 16, 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

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()`

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()`

`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()`

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

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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