Package ‘pogos’

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Title  PharmacOGenomics Ontology Support

Description  Provide simple utilities for querying bhklab PharmacoDB, modeling API outputs, and integrating to cell and compound ontologies.

Version  1.24.0

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Suggests  knitr, DT, ontologyPlot, testthat, rmarkdown, BiocStyle

Imports  methods, S4Vectors, utils, shiny, ontoProc, ggplot2, graphics

Depends  R (>= 3.5.0), rjson (>= 0.2.15), httr (>= 1.3.1)

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License  Artistic-2.0

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LazyData  yes

biocViews  Pharmacogenomics, PooledScreens, ImmunoOncology

RoxygenNote  7.2.3

VignetteBuilder  knitr

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## basicDecoder

*convert binary output of GET($content) to list*

### Description

convert binary output of GET($content) to list

### Usage

```r
basicDecoder(x)
```

### Arguments

- `x` : string suitable for input to `GET` as `GET(x)`

### Value

output of `fromJSON`, typically a list

### Examples

```r
c1 = basicDecoder('https://pharmacodb.pmggenomics.ca/api/v1/cell_lines')
unlist(c1)
```

## compoundsByCell

*initial version of compound browser over pharmacoDb cells*

### Description

initial version of compound browser over pharmacoDb cells

### Usage

```r
compoundsByCell()
```

### Value

only used for side effect of running shiny app
Note
Simple shiny app demonstrating coverage of PharmacoDb compounds by CHEBI. If a cell line selected is not present in selected dataset, the app will wait for a compatible selection to be made.

Examples
```r
if (!requireNamespace("shiny")) stop("install shiny to use compoundsByCell")
if (interactive()) print(compoundsByCell())
```

Description
compounds_v1: serialization of compounds info from PharmacoDb v1

Usage
compounds_v1
tissues_v1
cell_lines_v1
datasets_v1
CCLE_drts

Format
S4Vectors DataFrame instance
S4Vectors DataFrame instance
S4Vectors DataFrame instance
S4Vectors DataFrame instance
DRTraceSet instance

Source
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb April 2018
DRProfile-class

DRProfSet is a class for managing dose-response information about cell lines from a pharmacogenomics dataset.

Description

DRProfSet is a class for managing dose-response information about cell lines from a pharmacogenomics dataset.

getDrugs extracts drug list

DRProfSet manages all data from a given cell line from a pharmacogenomics source.

Usage

getDrugs(x)

DRProfSet(cell_line = "MCF7", dataset = "CCLE")

# S4 method for signature 'DRProfSet,missing'
plot(x, y, ...)

Arguments

x instance of DRProfSet
cell_line character(1) cell line name, entries in cell_lines_v1
dataset character(1) resource name, entries in datasets_v1
y for plot: not used
... not used

Value

getDrugs: character vector
instance of DRProfSet
DRTraceSet-class

Examples

```r
if (interactive()) trs = DRTraceSet() else trs = iriCCLE()
ps = traces(trs)[[1]]
ps
getDrugs(ps)
if (interactive()) DRProfSet()
```

DRTraceSet-class  
DRTraceSet class manages dose-response information for a single cell line, multiple drugs

Description

DRTraceSet class manages dose-response information for a single cell line, multiple drugs

DRTraceSet constructor for multiple cell lines, single drug, single dataset

Usage

```r
## S4 method for signature 'DRTraceSet,missing'
plot(x, y, ...)
DRTraceSet(
  cell_lines = c("SK-ES-1", "TC-71", "MHH-ES-1", "HCC-56", "SK-HEP-1"),
  drug = "Irinotecan",
  dataset = "CCLE"
)
```

Arguments

- `x` for plot: instance of DRTraceSet
- `y` for plot: not used
- `...` not used
- `cell_lines` character vector of cell line names, must be found in `cell_lines_v1` data of pogos package
- `drug` character(1) drug name in `compounds_v1`
- `dataset` character(1) dataset known to pharmacodb.pmgenomics.ca

Value

instance of DRTraceSet

Note

Will query pharmacodb for relevant dose-response information

Examples

```r
DRTraceSet()
```
**iriCCLE**

*obtain an example trace set stored locally, for irinotecan and selected cell lines*

**Description**

*obtain an example trace set stored locally, for irinotecan and selected cell lines*

**Usage**

`iriCCLE()`

**Value**

an instance of DRTraceSet

**Examples**

```r
iri = iriCCLE()
iri
plot(iri)
```

**rxdbQuery_v1**

*very simple query formulation, build queries using endpoints of bhklab PharmacoDB API*

**Description**

*very simple query formulation, build queries using endpoints of bhklab PharmacoDB API*

**Usage**

```r
rxdbQuery_v1(
    ..., url = "https://pharmacodb.pmgenomics.ca/api/v1/",
    decoder = basicDecoder
)
```

**Arguments**

- `...` typically a string representing an API endpoint, will be processed by unlist() and then to paste0 preceded by `url`
- `url` of a PharmacoDB server API target
- `decoder` a function of one argument that will be applied to API response (typically JSON)
topEndpoints_v1

Description
enumerate top level endpoint terms for bhklab PharmacoDB API

Usage
topEndpoints_v1()

Value
typically a list, dependent on decoder parameter

Examples
qout = rxdbQuery_v1('cell_lines') # yields 30; append '?all=true' to retrieve all
unlist(lapply(qout, function(x) x[[2]]))

---

traces

Description
trace extractor

Usage
traces(x)

Arguments
x instance of DRTraceSet

Value
a list of DRProfile instances
Examples

```r
iri = iriCLE()
str(traces(iri)[[1]])
```

Description

subscripting on DRProfSet extracts a profile for a single drug whose name constitutes the index

Usage

```r
## S4 method for signature 'DRProfSet,character,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

Arguments

- `x`: instance of DRProfSet
- `i`: character(1) drug name
- `j`: not used
- `...`: not used
- `drop`: logical(1) not used

Value

a DRProfSet instance restricted to experiments involving the selected drug
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