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.

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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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LazyData yes

biocViews Pharmacogenomics, PooledScreens, ImmunoOncology

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BasicDecoder

convert binary output of GET($content) to list

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

Usage
basicDecoder(x)

Arguments
x

string suitable for input to GET as GET(x)

Value
output of fromJSON, typically a list

Examples

cl = basicDecoder('https://pharmacodb.pmgenomics.ca/api/v1/cell_lines')
unlist(cl)

CompoundsByCell

initial version of compound browser over pharmacoDb cells

Description
initial version of compound browser over pharmacoDb cells

Usage
compoundsByCell()

Value
only used for side effect of running shiny app
**compounds_v1**

**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
Examples

data(compounds_v1)
head(compounds_v1)
data(tissues_v1)
head(tissues_v1)
data(cell_lines_v1)
head(cell_lines_v1)
data(datasets_v1)
head(datasets_v1)
data(CCLE_drts)
CCLE_drts

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

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**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
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, ...)
```

```r
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(
  ...,  # ... typically a string representing an API endpoint, will be processed by unlist() and then to paste0 preceded by url
  url = "https://pharmacodb.pmgenomics.ca/api/v1/",  # of a PharmacoDB server API target
  decoder = basicDecoder  # a function of one argument that will be applied to API response (typically JSON)
)
```
**topEndpoints_v1**

**Value**

typically a list, dependent on decoder parameter

**Examples**

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

---

**traces**

**Description**

trace extractor

**Usage**

```r
traces(x)
```

**Arguments**

- `x` instance of DRTraceSet

**Value**

a list of DRProfile instances
Examples

ir1 = ir1CCLE()
str(traces(ir1)[[1]])

Description

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

Usage

## 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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