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 1.17.0

Author Vince Carey <stvjc@channing.harvard.edu>

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)

Maintainer VJ Carey <stvjc@channing.harvard.edu>

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LazyData yes

biocViews Pharmacogenomics, PooledScreens, ImmunoOncology

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VignetteBuilder knitr

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R topics documented:

`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

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

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

`compounds_v1` *compounds_v1: serialization of compounds info from PharmacoDb v1*

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
```

`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

Examples

```
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

```
## 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

```
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

```
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

```
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)

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]]))
```

---

topEndpoints_v1 *enumerate top level endpoint terms for bhklab PharmacoDB API*

Description

enumerate top level endpoint terms for bhklab PharmacoDB API

Usage

```
topEndpoints_v1()
```

Value

a character vector of available endpoints

Examples

```
topEndpoints_v1()
```

---

traces *trace extractor*

Description

trace extractor

Usage

```
traces(x)
```

Arguments

x	instance of DRTraceSet

Value

a list of DRProfile instances

Examples

```
iri = iriCCLE()
str(traces(iri)[[1]])
```

`[,DRProfSet,character,ANY-method`
subscripting on DRProfSet extracts a profile for a single drug whose name constitutes the index

---

Description

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

Usage

```
## S4 method for signature 'DRProfSet,character,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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