Package ‘pogos’

March 1, 2024

Title PharmacOGenomics Ontology Support

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

Version 1.22.0

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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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LazyLoad yes

LazyData yes

biocViews Pharmacogenomics, PooledScreens, ImmunoOncology

RoxygenNote 7.2.3

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/pogos

git_branch RELEASE_3_18

git_last_commit 7f46f03

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-02-29

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### compoundsByCell

**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

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

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

```r
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

```r
getDrugs(x)

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

```r
## 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**

**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
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)
### topEndpoints_v1

**Value**

typically a list, dependent on decoder parameter

**Examples**

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

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<th>Description</th>
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<td><code>topEndpoints_v1</code></td>
<td>enumerate top level endpoint terms for bhklab PharmacoDB API</td>
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### traces

**Description**

trace extractor

**Usage**

```r
traces(x)
```

**Arguments**

- `x` instance of DRTraceSet

**Value**

- a list of DRProfile instances
Examples
iri = iriCCLE()
str(traces(iri)[[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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