Package 'RPharmacoDB'

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Title R interface to PharmacoDB

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Description

R interface for accessing PharmacoDB, an integrative repository of pharmacogenomic data

Depends R (>= 3.1.0), RCurl, RJSONIO, data.table, plyr

R topics documented:

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getAllCells *Obtain all cell lines tested on a set of drugs*

Description

Same as title

Usage

```
getAllCells(drug)
```

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Arguments

drug   [vector] vector of drugs to search

Value

list of data.frame or NA containing search results

Examples

```
getAllCells(c("Erlotinib", "17-AAG"))
```

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getAllDrugs   *Obtain all drugs tested on a set of cell lines*

Description

Same as title

Usage

```
getAllDrugs(cell)
```

Arguments

cell   [vector] vector of cell lines to search

Value

list of data.frame or NA containing search results

Examples

```
getAllDrugs(c("MCF7", "1321N1"))
```

---

getCuration   *Obtain a curation*

Description

getCuration requests a particular curation according to user specified parameters from Pharma-coDB web service.

Usage

```
getCuration(curation = c("cell", "drug", "tissue", "histology",
  "gene_expression"), study = NULL, subtype = NULL)
```

Arguments

curation	the curation to be requested:
	"cell" is listing of cell lines in each study and corresponding synonyms
	"drug" is listing of drugs in each study and corresponding synonyms "tissue" is listing of cell lines in each study, their corresponding tissue types, and matching of tissue types in each study to COSMIC tissue types
	"histology" is listing of cell lines in each study, their corresponding histological subtypes, matching between subtypes based on manual curation by BHK lab
	"gene_expression" is listing of gene expression metadata by study
study	optional vector of studies to subset curation '
subtype	optional vector of subtype so only curation for that subtype is displayed only valid for "tissue", "histology" and "gene expression" curations

Value

list containing curations if found or NA if curation not found

Examples

```
getCuration("cell")
## get the complete cell line curation
getCuration("drug", study=c("CGP", "CCLE"))
## get all drugs in CGP and in CCLE
getCuration("tissue", study=c("CCLE", "GRAY", "GNE"), subtype=c("breast", "testis"))
## get all breast and testis cancer cell lines tested in CCLE and GRAY
getCuration("histology", subtype = "carcinoma")
## get all cell lines which are carcinomas
getCuration("gene_expression", "MEIS")
## returns warning since "MEIS" study does not exist
```

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getDataset *Obtain a data set according to a study name*

Description

getDataset requests a particular dataset according to user specified study

Usage

```
getDataset(study, summary = FALSE, stats = NULL)
```

Arguments

study	[vector] vector of studies from which to obtain data
summary	[boolean] optional parameter of whether or not to return summary data if summary=TRUE, summary data is returned if summary=FALSE, dose response data is returned default is summary=FALSE
stats	[vector] vector of summary statistics values to return default is NULL because default for summary is FALSE

Value

list of data.frame containing data if found or NA if data does not exist

Examples

```
getDataset("CCLE") ## get the CCLE dose-response data
getDataset(c("CGP", "GNE")) ## get CGP and GNE dose-response data
getDataset("CTRP", summary=TRUE) ## get all summary statistics for CTRP data
getDataset("CGP", stats = c("IC50_published")) ## get IC50 values in CGP
```

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getDataStudies	*Get list of studies with dose-response data/summary data in the database*

Description

Same as title

Usage

```
getDataStudies()
```

Value

vector of studies

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getExpData	*Obtain a data set according to a study name*

Description

getExpData requests a particular dataset according to user specified study

Usage

```
getExpData(cellline = NULL, drug = NULL, summary = FALSE, stats = NULL)
```

Arguments

cellline	[vector] vector of cell lines for which to obtain data if cellline=NULL and drug != NULL, then data for all celllines tested on that vector of drugs is returned.
drug	[vector] vector of drugs for which to obtain data if drug=NULL and cellline != NULL, then data for all drugs tested on the cellline vector returned
	if drug!=NULL and cellline !=NULL, then data for all experiments in the set cellline, drug pairs for which there is data is returned
summary	[boolean] whether or not to return summary data if summary=TRUE, summary data is returned if summary=FALSE, dose response data is returned default is summary=FALSE
stats	[vector] vector of summary statistics values to return default is stats=NULL because summary=FALSE

Value

list of data.frame containing data if found or NA if data does not exist

Examples

```
getExpData(cellline="HCC70") ## get all dose-response curves tested on HCC70
## Get the published IC50 values for all cell lines tested on Erlotinib or 17-AAG
getExpData(drug=c("Erlotinib", "17-AAG"), stats = "IC50_Published"))
## Get all summary statistics for experiments tested on MCF7 and 1321N1
## and with erlotinib or 17-AAG
getExpData(cellline = c("MCF7", "1321N1"), drug = c("erlotinib", "17-AAG"), summary = TRUE)
```

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getStudies	*Get list of studies in the database*

Description

Same as title

Usage

```
getStudies()
```

Value

vector of studies

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listSummaryStats	*Get list of summary statistics available in a study*

Description

Same as title

Usage

```
listSummaryStats(study)
```

Value

list of vector of summary statistics

Examples

```
listSummaryStats(c("CCLE", "CGP"))
```

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