

Package ‘Rxnat’

September 15, 2020

Type Package

Version 1.0.14

Title Queries and Extracts Images from Extensible Neuroimaging Archive
Toolkit Public/Private Datasets

Description

Allows communication with Extensible Neuroimaging Archive Toolkit <<https://www.xnat.org>>. 'Rxnat' is using the 'XNAT' REST API to perform data queries and download images.

Maintainer Adi Gherman <adig@jhu.edu>

Imports RCurl, httr, utils, dplyr, tibble

Suggests testthat, knitr, rmarkdown, covr, scales, devtools

License GPL-2

Encoding UTF-8

LazyData true

ByteCompile true

RoxygenNote 7.1.1

VignetteBuilder knitr

BugReports <https://github.com/adigherman/Rxnat/issues>

NeedsCompilation no

Author Adi Gherman [aut, cre]

Repository CRAN

Date/Publication 2020-09-15 21:20:03 UTC

R topics documented:

download_xnat_dir	2
download_xnat_file	2
get_scan_resources	3
query_scan_resources	4
string2csv	4
xnat_connection	5

Index	6
--------------	----------

download_xnat_dir *Download XNAT directory*

Description

Download a full directory of data

Usage

```
download_xnat_dir(conn, ...)
```

Arguments

conn	The XNAT connection returned by a xnat_connect call
...	experiment_ID the experiment Id for which we need to download data scan_type type of image scan zipped zip the downloaded result verbose Should progress be added to download? error Should function error if download failed? extract Unzip the result and return the files list (based on scan_type)

Value

Display path to the downloaded file

Examples

```
## Not run: nitrc <- xnat_connect('https://nitrc.org/ir', xnat_name='NITRC')
## Not run: download_xnat_dir(nitrc,
                             experiment_ID='NITRC_IR_E10507',
                             scan_type='T2',
                             file_dir = tempdir(),
                             extract = TRUE)

## End(Not run)
```

download_xnat_file *Download XNAT file*

Description

Download a single file from XNAT

Usage

```
download_xnat_file(conn, ...)
```

Arguments

conn	The XNAT connection returned by a xnat_connect call
...	file_path Path to the file to be downloaded destfile Destination filename prefix Prefix the file name with this (prevents overwriting of same name files in case function is used to download multiple scan types at once) verbose Should progress be added to download? error Should function error if download failed?

Value

Display path to the downloaded file

Examples

```
## file_path is retrieved using the get_scan_resources() function
## Not run:
xnat_central_conn <- xnat_connect('https://central.xnat.org', xnat_name="CENTRAL")
r <- get_scan_resources(xnat_central_conn, 'CENTRAL_E00760')
download_xnat_file(xnat_central_conn, r$URI[1])

## End(Not run)
```

get_scan_resources *Get scan resources for a specific experiment ID*

Description

Get a full list of available resources for a specific experiment ID

Usage

```
get_scan_resources(conn, ...)
```

Arguments

conn	The XNAT connection returned by a xnat_connect call
...	experiment_ID the experiment ID identifier, unique for each individual subject

Examples

```
## Connect to XNAT CENTRAL
## Not run:
xnat_central_conn <- xnat_connect('https://central1.xnat.org', xnat_name="CENTRAL")
get_scan_resources(xnat_central_conn, 'CENTRAL_E00760')

## End(Not run)
```

query_scan_resources *Query all XNAT scan resources*

Description

Query all scan resources to match specific query parameters and return a list of all matching rows

Usage

```
query_scan_resources(conn, ...)
```

Arguments

conn	The XNAT connection returned by a xnat_connect call
...	Select query parameters: subject_ID, project, age, experiment_ID, type TR, TE, TI, flip, voxel_res, voxel_res_X, voxel_res_Y, voxel_res_Z, orientation

Value

A tibble containing all matching rows. XNAT does not do sql join joins so only one row is returned per match. However each of the experiment_IDs returned will have at least one row matching the user query (even if the displayed results show something else). This function should be used just to retrieve matching experiment IDs for downloading the queried data.

Examples

```
## Not run: hcp <-xnat_connect('https://db.humanconnectome.org', xnat_name = "hcp")
## Not run: query_scan_resources(hcp,age='26', project='HCP_500')
```

string2csv *Convert string to csv*

Description

Convert a string to csv format

Usage

```
string2csv(string)
```

Arguments

string	input string
--------	--------------

Examples

```
{
  string2csv("col1,col2,col3\ncell_1_1,cell_1_2,cell_1_3\ncell_2_1,cell_2_2,cell_2_3")
  string2csv("c1,c2,c3\n1,2,3")
}
```

xnat_connection	<i>Make a connection to an XNAT server</i>
-----------------	--

Description

Make the XNAT connection and provides functions to retrieve the list of projects, experiments and subjects.

Usage

```
xnat_connect(base_url, username = NULL, password = NULL, xnat_name = NULL)
```

Arguments

base_url	the URL for the XNAT server
username	user name to use for connection. If NULL this can be provided through the xxx_WEB_USER system variable where xxx is provided by the xnat_name parameter
password	user name to use for connection. If NULL this can be provided through the xxx_WEB_PASS system variable where xxx is provided by the xnat_name parameter
xnat_name	prefix to use for retrieving the proper username/pass system variables for a specific XNAT server

Value

projects

Examples

```
## Connect to the NITRC.ORG database
## Not run: xnat_connect('https://nitrc.org/ir', xnat_name='NITRC')

## Connect to the XNAT.CENTRAL database
## Not run: xnat_connect('https://central.xnat.org', xnat_name="CENTRAL")
```

Index

`download_xnat_dir`, [2](#)

`download_xnat_file`, [2](#)

`get_scan_resources`, [3](#)

`query_scan_resources`, [4](#)

`string2csv`, [4](#)

`xnat_connect (xnat_connection)`, [5](#)

`xnat_connection`, [5](#)