

Package ‘TCIApathfinder’

July 21, 2025

Title Client for the Cancer Imaging Archive REST API

Version 1.0.6

Description A wrapper for The Cancer Imaging Archive's REST API. The Cancer Imaging Archive (TCIA) hosts de-identified medical images of cancer available for public download, as well as rich metadata for each image series. TCIA provides a REST API for programmatic access to the data. This package provides simple functions to access each API endpoint. For more information, see <<https://github.com/pamelarussell/TCIApathfinder>> and TCIA's website.

Depends R (>= 3.4.0)

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Encoding UTF-8

LazyData true

Imports httr, jsonlite

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, oro.dicom, testthat

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2019-09-21 11:20:03 UTC

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get_body_part_names	<i>Get body part names</i>
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Description

Get body part names

Usage

get_body_part_names(collection = NULL, modality = NULL)

Arguments

- | | |
|------------|--|
| collection | TCIA collection name. If collection is NULL, body part names from all collections will be returned. To get a list of available collection names, call get_collection_names . |
| modality | Modality name. If modality is NULL, body part names from all modalities will be returned. To get a list of available modality names, call get_modality_names or see DICOM Modality Abbreviations . |

Value

- List containing elements:
- body_parts: character vector of body part names
 - content: parsed API response content
 - response: API response

See Also

[get_collection_names](#), [get_modality_names](#), [DICOM Modality Abbreviations](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_body_part_names()
get_body_part_names(collection = "TCGA-BRCA")
get_body_part_names(modality = "MR")
get_body_part_names(collection = "TCGA-BRCA", modality = "MR")

## End(Not run)
```

`get_collection_names` *Get the names of all TCIA collections*

Description

Get the names of all TCIA collections

Usage

```
get_collection_names()
```

Value

List containing elements:

- `collection_names`: character vector of TCIA collection names
- `content`: parsed API response content
- `response`: API response

See Also

[TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_collection_names()

## End(Not run)
```

get_manufacturer_names

Get manufacturer names

Description

Get manufacturer names

Usage

```
get_manufacturer_names(collection = NULL, modality = NULL,  
  body_part = NULL)
```

Arguments

collection	TCIA collection name. If collection is NULL, manufacturer names from all collections will be returned. To get a list of available collection names, call get_collection_names .
modality	Modality name. If modality is NULL, manufacturer names for all modalities will be returned. To get a list of available modality names, call get_modality_names or see DICOM Modality Abbreviations .
body_part	Body part name. If body_part is NULL, manufacturer names for all body parts will be returned. To get a list of available body part names, call get_body_part_names .

Value

List containing elements:

- manufacturer_names: character vector of manufacturer names
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [get_modality_names](#), [get_body_part_names](#), [DICOM Modality Abbreviations](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_manufacturer_names()  
get_manufacturer_names(collection = "TCGA-BRCA")  
get_manufacturer_names(collection = "TCGA-BRCA", modality = "MR", body_part = "BREAST")  
  
## End(Not run)
```

get_modality_names	<i>Get modality names</i>
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Description

Get modality names

Usage

```
get_modality_names(collection = NULL, body_part = NULL)
```

Arguments

collection	TCIA collection name. If collection is NULL, modality names from all collections will be returned. To get a list of available collection names, call get_collection_names .
body_part	Body part name. If body_part is NULL, modality names for all body parts will be returned. To get a list of available body part names, call get_body_part_names .

Value

List containing elements:

- modalities: character vector of modality names
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [get_body_part_names](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_modality_names()  
get_modality_names(collection = "TCGA-BRCA")  
get_modality_names(body_part = "BREAST")  
get_modality_names(collection = "TCGA-BRCA", body_part = "BREAST")  
  
## End(Not run)
```

`get_new_patients_in_collection`

Get IDs of patients that have been added to a collection since a specified date

Description

Get IDs of patients that have been added to a collection since a specified date

Usage

```
get_new_patients_in_collection(collection, date)
```

Arguments

collection	TCIA collection name. To get a list of available collection names, call get_collection_names .
date	Date in format "YYYY-MM-DD"

Value

List containing elements:

- patient_ids: Patient IDs
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_new_patients_in_collection("TCGA-BRCA", "2014-01-01")  
  
## End(Not run)
```

`get_new_studies_in_collection`

Get studies that have been added to a collection and optionally to a patient since a specified date

Description

Get studies that have been added to a collection and optionally to a patient since a specified date

Usage

```
get_new_studies_in_collection(collection, date, patient_id = NULL)
```

Arguments

<code>collection</code>	TCIA collection name. To get a list of available collection names, call get_collection_names .
<code>date</code>	Date in format "YYYY-MM-DD"
<code>patient_id</code>	Patient ID. To get a list of available patient IDs, call get_patient_info . If <code>patient_id</code> is NULL, relevant studies for all patients in the collection will be returned.

Value

List containing elements:

- `studies`: Data frame of collection, patient ID, and study instance UID
- `content`: parsed API response content
- `response`: API response

See Also

[get_collection_names](#), [get_patient_info](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_new_studies_in_collection("TCGA-BRCA", "2014-01-01")  
get_new_studies_in_collection("TCGA-BRCA", "2014-01-01", "TCGA-OL-A660")  
  
## End(Not run)
```

`get_patients_by_modality`*Get patient IDs given a collection name and modality*

Description

Get patient IDs given a collection name and modality

Usage

```
get_patients_by_modality(collection, modality)
```

Arguments

collection	TCIA collection name. To get a list of available collection names, call get_collection_names .
modality	Modality name. To get a list of available modality names, call get_modality_names or see DICOM Modality Abbreviations .

Value

List containing elements:

- patient_ids: Patient IDs
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [get_modality_names](#), [DICOM Modality Abbreviations](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_patients_by_modality("TCGA-BRCA", "MR")  
  
## End(Not run)
```

get_patient_info	<i>Get patient information</i>
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Description

Get patient information

Usage

```
get_patient_info(collection = NULL)
```

Arguments

collection	TCIA collection name. If collection is NULL, patients from all collections will be returned. To get a list of available collection names, call get_collection_names .
------------	---

Value

List containing elements:

- patients: Data frame of patient ID, name, sex, ethnic group, and collection name
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_patient_info()  
get_patient_info("TCGA-BRCA")  
  
## End(Not run)
```

get_patient_studies	<i>Get patient study information</i>
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Description

Get patient study information

Usage

```
get_patient_studies(collection = NULL, patient_id = NULL,
  study_instance_uid = NULL)
```

Arguments

collection	TCIA collection name. To get a list of available collection names, call get_collection_names . If collection is NULL, information for all relevant collections will be returned.
patient_id	Patient ID. To get a list of available patient IDs, call get_patient_info . If patient_id is NULL, information for all relevant patients will be returned.
study_instance_uid	Study instance UID. If study_instance_uid is NULL, information for all relevant study instance UIDs will be returned. To get available study instance UIDs, call get_studies_in_collection , get_patient_studies , or get_new_studies_in_collection .

Value

List containing elements:

- patient_studies: Data frame with columns representing the contents of a PatientStudy object as described in [TCIA API Return Values](#)
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [get_patient_info](#), [get_studies_in_collection](#), [get_patient_studies](#), [get_new_studies_in_collection](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_patient_studies()
get_patient_studies(collection = "TCGA-BRCA")
get_patient_studies(patient_id = "TCGA-OL-A6V0")
get_patient_studies(patient_id = "TCGA-OL-A5DA",
  study_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.104582989590517557856962159716")

## End(Not run)
```

get_series_info	<i>Get image series information</i>
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Description

Get image series information

Usage

```
get_series_info(collection = NULL, patient_id = NULL,
               study_instance_uid = NULL, series_instance_uid = NULL,
               modality = NULL, body_part_examined = NULL,
               manufacturer_model_name = NULL, manufacturer = NULL)
```

Arguments

collection	TCIA collection name. To get a list of available collection names, call get_collection_names . If collection is NULL, information for all relevant collections will be returned.
patient_id	Patient ID. To get a list of available patient IDs, call get_patient_info . If patient_id is NULL, information for all relevant patients will be returned.
study_instance_uid	Study instance UID. If study_instance_uid is NULL, information for all relevant study instance UIDs will be returned. To get available study instance UIDs, call get_studies_in_collection , get_patient_studies , or get_new_studies_in_collection .
series_instance_uid	Series instance UID. To get a list of available series instance UIDs, call this function leaving out parameter series_instance_uid. If series_instance_uid is NULL, information for all relevant series will be returned.
modality	Modality name. To get a list of available modality names, call get_modality_names or see DICOM Modality Abbreviations . If modality is NULL, information for all relevant modalities will be returned.
body_part_examined	Body part name. To get a list of available body part names, call get_body_part_names . If body_part_examined is NULL, information for all relevant body parts will be returned. IMPORTANT: a bug in this query key has been observed in the TCIA API. If queries using this key return zero results, try removing this parameter.
manufacturer_model_name	Manufacturer model name. To get a list of available model names, call this function leaving out parameter manufacturer_model_name. If manufacturer_model_name is NULL, information for all relevant model names will be returned.
manufacturer	Manufacturer name. To get a list of available manufacturer names, call get_manufacturer_names . If manufacturer is NULL, information for all relevant manufacturers will be returned.

Value

List containing elements:

- series: Data frame with columns representing the contents of a Series object as described in [TCIA API Return Values](#)
- content: parsed API response content
- response: API response

See Also

[get_collection_names](#), [get_patient_info](#), [get_studies_in_collection](#), [get_patient_studies](#), [get_new_studies_in_collection](#), [get_modality_names](#), [get_body_part_names](#), [get_manufacturer_names](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_series_info()
get_series_info(collection = "TCGA-BRCA")
get_series_info(patient_id = "TCGA-OL-A6V0")
get_series_info(modality = "MR", manufacturer = "GE MEDICAL SYSTEMS")

## End(Not run)
```

get_series_size	<i>Get size of image series</i>
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Description

Get size of image series

Usage

```
get_series_size(series_instance_uid)
```

Arguments

series_instance_uid
Series instance UID. To get a list of available series instance UIDs, call [get_series_info](#).

Value

List containing elements:

- size_bytes: Total size of image series in bytes
- object_count: Number of objects in image series
- content: parsed API response content
- response: API response

See Also

[get_series_info](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_series_size("1.3.6.1.4.1.14519.5.2.1.5382.4002.272234209223992578700978260744")

## End(Not run)
```

`get_sop_instance_uids` *Get SOP instance UUIDs (individual DICOM image IDs) for an image series*

Description

Get SOP instance UUIDs (individual DICOM image IDs) for an image series

Usage

```
get_sop_instance_uids(series_instance_uid)
```

Arguments

`series_instance_uid`
Series instance UID. To get a list of available series instance UUIDs, call [get_series_info](#).

Value

List containing elements:

- `sop_instance_uids`: character vector of SOP instance UUIDs (individual DICOM image IDs)
- `content`: parsed API response content
- `response`: API response

See Also

[get_series_info](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
get_sop_instance_uids("1.3.6.1.4.1.14519.5.2.1.5382.4002.272234209223992578700978260744")

## End(Not run)
```

`get_studies_in_collection`*Get studies in a collection and optionally for a specific patient*

Description

Get studies in a collection and optionally for a specific patient

Usage

```
get_studies_in_collection(collection, patient_id = NULL)
```

Arguments

<code>collection</code>	TCIA collection name. To get a list of available collection names, call get_collection_names .
<code>patient_id</code>	Patient ID. To get a list of available patient IDs, call get_patient_info . If <code>patient_id</code> is NULL, studies for all patients in the collection will be returned.

Value

List containing elements:

- `studies`: Data frame of collection, patient ID, and study instance UID
- `content`: parsed API response content
- `response`: API response

See Also

[get_collection_names](#), [get_patient_info](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
get_studies_in_collection("TCGA-BRCA")  
get_studies_in_collection("TCGA-BRCA", "TCGA-OL-A660")  
  
## End(Not run)
```

`save_extracted_image_series`*Save a series of DICOM image files to a directory*

Description

Save a series of DICOM image files to a directory

Usage

```
save_extracted_image_series(series_instance_uid, out_dir = NULL,  
    verbose = TRUE)
```

```
extract_image_series(zip_file, out_dir = NULL)
```

Arguments

`series_instance_uid`

Series instance UID. To get a list of available series instance UIDs, call [get_series_info](#).
Note: if `series_instance_uid` is invalid, the API may still successfully return an empty zip file.

`out_dir` Directory to write zip file to

`verbose` print diagnostic messages

`zip_file` downloaded zip file, usually output of [save_image_series](#)

Value

List containing elements:

- `files`: The output zip file that was written
- `dirs`: Directories of the files
- `out_file`: The output zip file that was written
- `response`: API response

Examples

```
## Not run:  
save_extracted_image_series(  
    series_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.806935685832642465081499816867")  
  
## End(Not run)
```

save_image_series	<i>Save a series of DICOM image files as a zip file</i>
-------------------	---

Description

Save a series of DICOM image files as a zip file

Usage

```
save_image_series(series_instance_uid, out_dir = NULL,
                  out_file_name = NULL)
```

Arguments

series_instance_uid	Series instance UID. To get a list of available series instance UIDs, call get_series_info . Note: if series_instance_uid is invalid, the API may still successfully return an empty zip file.
out_dir	Directory to write zip file to
out_file_name	Name of zip file to write. If out_file_name is NULL, the original file name will be used.

Value

List containing elements:

- out_file: The output zip file that was written
- response: API response

See Also

[get_series_info](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:
save_image_series(
  series_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.806935685832642465081499816867",
  out_dir = "~/Desktop")
save_image_series(
  series_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.806935685832642465081499816867",
  out_dir = "~/Desktop", out_file_name = "file.zip")

## End(Not run)
```

save_single_image	Save a single DICOM image file
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Description

Save a single DICOM image file

Usage

```
save_single_image(series_instance_uid, sop_instance_uid, out_dir = NULL,  
                  out_file_name = NULL)
```

Arguments

series_instance_uid	Series instance UID. To get a list of available series instance UIDs, call get_series_info .
sop_instance_uid	SOP instance UID. To get a list of SOP instance UIDs for an image series, call get_sop_instance_uids .
out_dir	Directory to write DICOM file to
out_file_name	Name of DICOM file to write, with .dcm extension. If out_file_name is NULL, the original file name will be used.

Value

List containing elements:

- out_file: The output file that was written
- response: API response

See Also

[get_series_info](#), [get_sop_instance_uids](#), [TCIA REST API Usage Guide](#), [TCIA API object definitions](#)

Examples

```
## Not run:  
save_single_image(  
  series_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.806935685832642465081499816867",  
  sop_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.257663256941568276393774062283")  
save_single_image(  
  series_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.806935685832642465081499816867",  
  sop_instance_uid = "1.3.6.1.4.1.14519.5.2.1.5382.4002.257663256941568276393774062283",  
  out_file_name = "file.dcm")  
  
## End(Not run)
```

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