Package ‘TCIApathfinder’

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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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LazyData true

Imports httr, jsonlite

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R topics documented:

`get_body_part_names` *Get body part names*

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` *Get modality names*

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

`collection`	TCIA collection name. To get a list of available collection names, call `get_collection_names`.
`date`	Date in format "YYYY-MM-DD"
`patient_id`	Patient ID. To get a list of available patient IDs, call `get_patient_info`. If `patient_id` 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-A66O")

## 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` *Get patient information*

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` *Get patient study information*

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-A6VO")
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` *Get image series information*

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-A6VO")
get_series_info(modality = "MR", manufacturer = "GE MEDICAL SYSTEMS")

## End(Not run)
```

`get_series_size` *Get size of image series*

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 UIDs (individual DICOM image IDs) for an image series*

Description

Get SOP instance UIDs (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 UIDs, call `get_series_info`.

Value

List containing elements:

- `sop_instance_uids`: character vector of SOP instance UIDs (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

`collection`	TCIA collection name. To get a list of available collection names, call `get_collection_names`.
`patient_id`	Patient ID. To get a list of available patient IDs, call `get_patient_info`. If `patient_id` 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-A66O")

## 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` *Save a series of DICOM image files as a zip file*

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*

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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