

Package ‘GenomicDataCommons’

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Author Martin Morgan [aut],
Davis Sean [aut, cre]

Maintainer Davis Sean <sdavis2@mail.nih.gov>

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aggregations

aggregations

Description

aggregations

Usage

aggregations(x)

```
## S3 method for class 'GDCQuery'
```

aggregations(x)

```
## S3 method for class 'GDCResponse'
```

aggregations(x)

Arguments

x a [GDCQuery](#) object

Value

a list of `data.frame` with one member for each requested facet. The data frames each have two columns, `key` and `doc_count`.

Methods (by class)

- GDCQuery:
- GDCResponse:

Examples

```
library(magrittr)
# Number of each file type
res = files() %>% facet(c('type', 'data_type')) %>% aggregations()
res$type
```

available_expand	<i>Return valid values for "expand"</i>
------------------	---

Description

The GDC allows a shorthand for specifying groups of fields to be returned by the metadata queries. These can be specified in a [select](#) method call to easily supply groups of fields.

Usage

```
available_expand(entity)

## S3 method for class 'character'
available_expand(entity)

## S3 method for class 'GDCQuery'
available_expand(entity)
```

Arguments

entity Either a [GDCQuery](#) object or a character(1) specifying a GDC entity ('cases', 'files', 'annotations', 'projects')

Value

A character vector

See Also

See https://docs.gdc.cancer.gov/API/Users_Guide/Search_and_Retrieval/#expand for details

Examples

```
head(available_expand('files'))
```

available_fields *S3 Generic to return all GDC fields*

Description

S3 Generic to return all GDC fields

Usage

```
available_fields(x)

## S3 method for class 'GDCQuery'
available_fields(x)

## S3 method for class 'character'
available_fields(x)
```

Arguments

x A character(1) string ('cases', 'files', 'projects', 'annotations') or an subclass of [GDCQuery](#).

Value

a character vector of the default fields

Methods (by class)

- GDCQuery: GDCQuery method
- character: character method

Examples

```
available_fields('projects')
projQuery = query('projects')
available_fields(projQuery)
```

available_values *Find common values for a GDC field*

Description

Find common values for a GDC field

Usage

```
available_values(entity, field, legacy = FALSE)
```

Arguments

entity	character(1), a GDC entity ("cases", "files", "annotations", "projects")
field	character(1), a field that is present in the entity record
legacy	logical(1), use the legacy endpoint or not.

Value

character vector of the top 100 (or fewer) most frequent values for a the given field

Examples

```
available_values('files', 'cases.project.project_id')[1:5]
```

count	<i>provide count of records in a GDCQuery</i>
-------	---

Description

provide count of records in a [GDCQuery](#)

Usage

```
count(x, ...)
```

```
## S3 method for class 'GDCQuery'
count(x, ...)
```

```
## S3 method for class 'GDCResponse'
count(x, ...)
```

Arguments

x	a GDCQuery object
...	passed to httr (good for passing config info, etc.)

Value

integer(1) representing the count of records that will be returned by the current query

Methods (by class)

- [GDCQuery](#):
- [GDCResponse](#):

Examples

```
# total number of projects
projects() %>% count()

# total number of cases
cases() %>% count()
```

default_fields	<i>S3 Generic to return default GDC fields</i>
----------------	--

Description

S3 Generic to return default GDC fields

Usage

```
default_fields(x)

## S3 method for class 'character'
default_fields(x)

## S3 method for class 'GDCQuery'
default_fields(x)
```

Arguments

x A character string ('cases', 'files', 'projects', 'annotations') or an subclass of [GDCQuery](#).

Value

a character vector of the default fields

Methods (by class)

- character: character method
- GDCQuery: GDCQuery method

Examples

```
default_fields('projects')
projQuery = query('projects')
default_fields(projQuery)
```

entity_name	<i>Get the entity name from a GDCQuery object</i>
-------------	---

Description

An "entity" is simply one of the four medata endpoints.

- cases
- projects
- files
- annotations

All [GDCQuery](#) objects will have an entity name. This S3 method is simply a utility accessor for those names.

Usage

```
entity_name(x)

## S3 method for class 'GDCQuery'
entity_name(x)

## S3 method for class 'GDCResults'
entity_name(x)
```

Arguments

x a [GDCQuery](#) object

Value

character(1) name of an associated entity; one of "cases", "files", "projects", "annotations".

Examples

```
qcases = cases()
qprojects = projects()

entity_name(qcases)
entity_name(qprojects)
```

expand	<i>Set the expand parameter</i>
--------	---------------------------------

Description

S3 generic to set GDCQuery expand parameter

Usage

```
expand(x, expand)

## S3 method for class 'GDCQuery'
expand(x, expand)
```

Arguments

x the objects on which to set fields
expand a character vector specifying the fields

Value

A [GDCQuery](#) object, with the expand member altered.

Methods (by class)

- GDCQuery: set expand fields on a GDCQuery object

Examples

```

gProj = projects()
gProj$fields
head(available_fields(gProj))
default_fields(gProj)

gProj %>%
  select(default_fields(gProj)[1:2]) %>%
  response() %>%
  str(max_level=2)

```

facet	<i>Set facets for a GDCQuery</i>
-------	--

Description

Set facets for a [GDCQuery](#)

Get facets for a [GDCQuery](#)

Usage

```

facet(x, facets)

get_facets(x)

## S3 method for class 'GDCQuery'
get_facets(x)

```

Arguments

x	a GDCQuery object
facets	a character vector of fields that will be used for forming aggregations (facets). Default is to set facets for all default fields. See default_fields for details

Value

returns a [GDCQuery](#) object, with facets field updated.

Examples

```

# create a new GDCQuery against the projects endpoint
gProj = projects()

# default facets are NULL
get_facets(gProj)

# set facets and save result
gProjFacet = facet(gProj)

# check facets
get_facets(gProjFacet)

```



```
# and get a response, noting that
# the aggregations list member contains
# tibbles for each facet
str(response(gProjFacet,size=2),max.level=2)
```

filtering

Manipulating GDCQuery filters

Description

Manipulating GDCQuery filters

The filter is simply a safe accessor for the filter element in [GDCQuery](#) objects.

The get_filter is simply a safe accessor for the filter element in [GDCQuery](#) objects.

Usage

```
filter(x, expr)
```

```
## S3 method for class 'GDCQuery'
filter(x, expr)
```

```
get_filter(x)
```

```
## S3 method for class 'GDCQuery'
get_filter(x)
```

Arguments

x	the object on which to set the filter list member
expr	a filter expression in the form of the right hand side of a formula, where bare names (without quotes) are allowed if they are available fields associated with the GDCQuery object, x

Value

A [GDCQuery](#) object with the filter field replaced by specified filter expression

Examples

```
# make a GDCQuery object to start
#
# Projects
#
pQuery = projects()

# check for the default fields
# so that we can use one of them to build a filter
default_fields(pQuery)
pQuery = filter(pQuery,~ project_id == 'TCGA-LUAC')
get_filter(pQuery)
```

```

#
# Files
#
fQuery = files()
default_fields(fQuery)

fQuery = filter(fQuery, ~ data_format == 'VCF')
get_filter(fQuery)

fQuery = filter(fQuery, ~ data_format == 'VCF' & experimental_strategy == 'WXS' & type == 'simple_somatic_muta

# Use str() to get a cleaner picture
str(get_filter(fQuery))

```

gdcdata

*Download GDC files***Description**

Download one or more files from GDC. Files are downloaded using the UUID and renamed to the file name on the remote system. By default, neither the uuid nor the file name on the remote system can exist.

Usage

```
gdcdata(uuids, destination_dir = tempfile(), overwrite = FALSE,
        progress = interactive(), token = NULL)
```

Arguments

uuids	character() of GDC file UUIDs.
destination_dir	character(1) file path to a directory for downloading files.
overwrite	logical(1) default FALSE indicating whether existing files with identical name should be over-written.
progress	logical(1) default TRUE in interactive sessions, FALSE otherwise indicating whether a progress par should be produced for each file download.
token	(optional) character(1) security token allowing access to restricted data. See https://gdc-docs.nci.nih.gov/API/Users_Guide/Authentication_and_Authorization/ .

Details

This function is appropriate for one or several files; for large downloads use [manifest](#) to create a manifest for and the GDC Data Transfer Tool.

Value

a named vector with file uuids as the names and paths as the value

See Also

[manifest](#) for downloading large data.

Examples

```
uuids <- c("e3228020-1c54-4521-9182-1ea14c5dc0f7",
           "18e1e38e-0f0a-4a0e-918f-08e6201ea140")
(files <- gdcdata(uuids, overwrite=TRUE))
setNames(file.size(files), names(files))
```

gdc_client	<i>return gdc-client executable path</i>
------------	--

Description

This function is a convenience function to find and return the path to the GDC Data Transfer Tool executable assumed to be named 'gdc-client'. The assumption is that the appropriate version of the GDC Data Transfer Tool is a separate download available from <https://gdc.cancer.gov/access-data/gdc-data-transfer-tool> and as a backup from <https://github.com/NCI-GDC/gdc-client>. The following locations are checked:

Usage

```
gdc_client()
```

Details

- Sys.which() to see if gdc-client is on the path
- The current working directory
- The file name specified in the environment variable GDC_CLIENT

Value

character(1) the path to the gdc-client executable.

Examples

```
# this cannot run without first
# downloading the GDC Data Transfer Tool
gdc_client = try(gdc_client(), silent=TRUE)
```

gdc_token	<i>return a gdc token from file or environment</i>
-----------	--

Description

The GDC requires an auth token for downloading data that are "controlled access". For example, BAM files for human datasets, germline variant calls, and SNP array raw data all are protected as "controlled access". For these files, a GDC access token is required. See the https://docs.gdc.cancer.gov/Data_Portal/Users_Guide/Authentication/#gdc-authentication-tokens. Note that this function simply returns a string value. It is possible to keep the GDC token in a variable in R or to pass a string directly to the appropriate parameter. This function is simply a convenience function for alternative approaches to get a token from an environment variable or a file.

Usage

```
gdc_token()
```

Details

This function will resolve locations of the GDC token in the following order:

- from the environment variable, GDC_TOKEN, expected to contain the token downloaded from the GDC as a string
- using `readLines` to read a file named in the environment variable, GDC_TOKEN_FILE
- using `readLines` to read from a file called `.gdc_token` in the user's home directory

If all of these fail, this function will return an error.

Value

character(1) (invisibly, to protect against inadvertently printing) the GDC token.

References

https://docs.gdc.cancer.gov/Data_Portal/Users_Guide/Authentication/#gdc-authentication-tokens

Examples

```
# This will not run before a GDC token  
# is in place.  
token = try(gdc_token(), silent=TRUE)
```

GenomicDataCommons *ncigdc: A package for computing the notorious bar statistic.*

Description

Cool package for interfacing with NCI GDC

finding data

- [query](#)
- [cases](#)
- [projects](#)
- [files](#)
- [annotations](#)
- [mapping](#)

downloading data

data

`grep_fields` *Find matching field names*

Description

This utility function allows quick text-based search of available fields for using [grep](#)

Usage

```
grep_fields(entity, pattern, ..., value = TRUE)
```

Arguments

<code>entity</code>	one of "files", "cases", "annotations", "projects" against which to gather available fields for matching
<code>pattern</code>	A regular expression that will be used in a call to grep
<code>...</code>	passed on to grep
<code>value</code>	<code>logical(1)</code> whether to return values as opposed to indices (passed along to grep)

Value

`character()` vector of field names matching pattern

Examples

```
grep_fields('files', 'analysis')
```

ids	<i>Get the ids associated with a GDC query or response</i>
-----	--

Description

The GDC assigns ids (in the form of uuids) to objects in its database. Those ids can be used for relationships, searching on the website, and as unique ids. All

Usage

```
ids(x)

## S3 method for class 'GDCQuery'
ids(x)

## S3 method for class 'GDCResults'
ids(x)

## S3 method for class 'GDCResponse'
ids(x)
```

Arguments

x A [GDCQuery](#) or [GDCResponse](#) object

Value

a character vector of all the entity ids

Examples

```
# use with a GDC query, in this case for "cases"
ids(cases() %>% filter(~ project.project_id == "TCGA-CHOL"))
# also works for responses
ids(response(files()))
# and results
ids(results(cases()))
```

id_field	<i>get the name of the id field</i>
----------	-------------------------------------

Description

In many places in the GenomicDataCommons package, the entity ids are stored in a column or a vector with a specific name that corresponds to the field name at the GDC. The format is the entity name (singular) "_id". This generic simply returns that name from a given object.

Usage

```
id_field(x)

## S3 method for class 'GDCQuery'
id_field(x)

## S3 method for class 'GDCResults'
id_field(x)
```

Arguments

x An object representing the query or results of an entity from the GDC ("cases", "files", "annotations", "projects")

Value

character(1) such as "case_id", "file_id", etc.

Methods (by class)

- GDCQuery: GDCQuery method
- GDCResults: GDCResults method

Examples

```
id_field(cases())
```

make_filter

Create NCI GDC filters for limiting GDC query results

Description

Searching the NCI GDC allows for complex filtering based on logical operations and simple comparisons. This function facilitates writing such filter expressions in R-like syntax with R code evaluation.

Usage

```
make_filter(expr, available_fields)
```

Arguments

expr a filter expression

available_fields a character vector of the additional names that will be injected into the filter evaluation environment

Details

If used with available_fields, "bare" fields that are named in the available_fields character vector can be used in the filter expression without quotes.

Value

a list that represents an R version of the JSON that will ultimately be used in an NCI GDC search or other query.

manifest	<i>Prepare GDC manifest file for bulk download</i>
----------	--

Description

The manifest function/method creates a manifest of files to be downloaded using the GDC Data Transfer Tool. There are methods for creating manifest data frames from [GDCQuery](#) objects that contain file information ("cases" and "files" queries).

Usage

```
manifest(x, from = 0, size = count(x), ...)
```

```
## S3 method for class 'gdc_files'
manifest(x, from = 0, size = count(x), ...)
```

```
## S3 method for class 'GDCfilesResponse'
manifest(x, from = 0, size = count(x), ...)
```

```
## S3 method for class 'GDCcasesResponse'
manifest(x, from = 0, size = count(x), ...)
```

Arguments

x	An GDCQuery object of subclass "gdc_files" or "gdc_cases".
from	Record number from which to start when returning the manifest.
size	The total number of records to return. Default will return the usually desirable full set of records.
...	passed to PUT .

Value

A [tibble](#), also of type "gdc_manifest", with five columns:

- id
- filename
- md5
- size
- state

Methods (by class)

- gdc_files:
- GDCfilesResponse:
- GDCcasesResponse:

Examples

```
gFiles = files()
shortManifest = gFiles %>% manifest(size=10)
head(shortManifest,n=3)
```

mapping

Query GDC for available endpoint fields

Description

Query GDC for available endpoint fields

Usage

```
mapping(endpoint)
```

Arguments

`endpoint` character(1) corresponding to endpoints for which users may specify additional or alternative fields. Endpoints include “projects”, “cases”, “files”, and “annotations”.

Value

A data frame describing the field (field name), full (full data model name), type (data type), and four additional columns describing the “set” to which the fields belong—“default”, “expand”, “multi”, and “nested”.

Examples

```
map <- mapping("projects")
head(map)
# get only the "default" fields
subset(map,defaults)
# And get just the text names of the "default" fields
subset(map,defaults)$field
```

query

Start a query of GDC metadata

Description

The basis for all functionality in this package starts with constructing a query in R. The `GDCQuery` object contains the filters, facets, and other parameters that define the returned results. A token is required for accessing certain datasets.

Usage

```
query(entity, filters = NULL, facets = NULL, legacy = FALSE,
      expand = NULL, fields = default_fields(entity))
```

```
cases(...)
```

```
files(...)
```

```
projects(...)
```

```
annotations(...)
```

Arguments

entity	character vector of 'cases', 'files', 'annotations', or 'projects'
filters	a filter list, typically created using <code>make_filter</code> , or added to an existing GDCQuery object using <code>filter</code> .
facets	a character vector of
legacy	logical(1) whether to use the "legacy" archive or not. See https://docs.gdc.cancer.gov/Data_Portal/Users_Guide/Legacy_Archive/ and https://gdc-portal.nci.nih.gov/legacy-archive/search/f for details.
expand	a character vector of "expands" to include in returned data
fields	a character vector of fields to return
...	passed through to <code>query</code>

Value

An S3 object, the GDCQuery object. This is a list with the following members.

- filters
- facets
- fields
- expand
- archive
- token

Functions

- `cases`: convenience constructor for a GDCQuery for cases
- `files`: convenience constructor for a GDCQuery for cases
- `projects`: convenience constructor for a GDCQuery for cases
- `annotations`: convenience constructor for a GDCQuery for annotations

Examples

```
qcases = query('cases')
# equivalent to:
qcases = cases()
```

readDNACopy	<i>Read DNACopy results into GRanges object</i>
-------------	---

Description

Read DNACopy results into GRanges object

Usage

```
readDNACopy(fname, ...)
```

Arguments

fname	The path to a DNACopy-like file.
...	passed to <code>read_tsv</code>

Value

a `GRanges` object

Examples

```
fname = system.file(package='GenomicDataCommons',
                    'extdata/dnacopy.tsv.gz')
dnac = readDNACopy(fname)
class(dnac)
length(dnac)
```

readHTSeqFile	<i>Read a single htseq-counts result file.</i>
---------------	--

Description

The htseq package is used extensively to count reads relative to regions (see <http://www-huber.embl.de/HTSeq/doc/counting.html>). The output of htseq-count is a simple two-column table that includes features in column 1 and counts in column 2. This function simply reads in the data from one such file and assigns column names.

Usage

```
readHTSeqFile(fname, samplename = "sample", ...)
```

Arguments

fname	character(1), the path of the htseq-count file.
samplename	character(1), the name of the sample. This will become the name of the second column on the resulting data.frame, making for easier merging if necessary.
...	passed to <code>read_tsv</code>

Value

a two-column data frame

Examples

```
fname = system.file(package='GenomicDataCommons',
                    'extdata/example.htseq.counts.gz')
dat = readHTSeqFile(fname)
head(dat)
```

response

Fetch [GDCQuery](#) metadata from GDC

Description

Fetch [GDCQuery](#) metadata from GDC

Usage

```
response(x, ...)

## S3 method for class 'GDCQuery'
response(x, from = 0, size = 10, ...,
        response_handler = jsonlite::fromJSON)

response_all(x, ...)
```

Arguments

x a [GDCQuery](#) object

... passed to `httr` (good for passing config info, etc.)

from integer index from which to start returning data

size number of records to return

response_handler a function that processes JSON (as text) and returns an R object. Default is [fromJSON](#).

Value

A `GDCResponse` object which is a list with the following members:

- results
- query
- aggregations
- pages

Examples

```
# basic class stuff
gCases = cases()
resp = response(gCases)
class(resp)
names(resp)

# And results from query
resp$results[[1]]
```

results

results

Description

results

Usage

```
results(x, ...)
```

S3 method for class 'GDCQuery'

```
results(x, ...)
```

S3 method for class 'GDCResponse'

```
results(x, ...)
```

Arguments

x a [GDCQuery](#) object

... passed on to [response](#)

Value

A (typically nested) list of GDC records

Methods (by class)

- GDCQuery:
- GDCResponse:

Examples

```
qcases = cases() %>% results()
length(qcases)
```

results_all	<i>results_all</i>
-------------	--------------------

Description

results_all

Usage

```
results_all(x)
```

```
## S3 method for class 'GDCQuery'
results_all(x)
```

```
## S3 method for class 'GDCResponse'
results_all(x)
```

Arguments

x a [GDCQuery](#) object

Value

A (typically nested) list of GDC records

Methods (by class)

- GDCQuery:
- GDCResponse:

Examples

```
# details of all available projects
projResults = projects() %>% results_all()
length(projResults)
count(projects())
```

select	<i>S3 generic to set GDCQuery fields</i>
--------	--

Description

S3 generic to set GDCQuery fields

Usage

```
select(x, fields)
```

```
## S3 method for class 'GDCQuery'
select(x, fields)
```

Arguments

x	the objects on which to set fields
fields	a character vector specifying the fields

Value

A [GDCQuery](#) object, with the fields member altered.

Methods (by class)

- GDCQuery: set fields on a GDCQuery object

Examples

```
gProj = projects()
gProj$fields
head(available_fields(gProj))
default_fields(gProj)

gProj %>%
  select(default_fields(gProj)[1:2]) %>%
  response() %>%
  str(max_level=2)
```

slicing

Query GDC for data slices

Description

This function returns a BAM file representing reads overlapping regions specified either as chromosomal regions or as gencode gene symbols.

Usage

```
slicing(uuid, regions, symbols, destination = tempfile(), overwrite = FALSE,
  progress = interactive(), token = NULL, legacy = FALSE)
```

Arguments

uuid	character(1) identifying the BAM file resource
regions	character() vector describing chromosomal regions, e.g., c("chr1", "chr2:10000", "chr3:10000-20000") (all of chromosome 1, chromosome 2 from position 10000 to the end, chromosome 3 from 10000 to 20000).
symbols	character() vector of gencode gene symbols, e.g., c("BRCA1", "PTEN")
destination	character(1) default tempfile() file path for BAM file slice
overwrite	logical(1) default FALSE can destination be overwritten?
progress	logical(1) default interactive() should a progress bar be used?

token	character(1) security token allowing access to restricted data. Almost all BAM data is restricted, so a token is usually required. See https://gdc-docs.nci.nih.gov/API/Users_Guide/Authentication_and_Authorization/ .
legacy	logical(1) whether or not to use the "legacy" archive, containing older, non-harmonized data.

Value

character(1) destination to the downloaded BAM file

Examples

```
slicing("df80679e-c4d3-487b-934c-fcc782e5d46e",
        regions="chr17:75000000-76000000",
        token=gdc_token())
```

status

Query the GDC for current status

Description

Query the GDC for current status

Usage

```
status(version = NULL)
```

Arguments

version (optional) character(1) version of GDC

Value

List describing current status.

Examples

```
status()
```

transfer	<i>Bulk data download</i>
----------	---------------------------

Description

The GDC maintains a special tool, https://docs.gdc.cancer.gov/Data_Transfer_Tool/Users_Guide/Getting_Started/, that enables high-performance, potentially parallel, and resumable downloads. The Data Transfer Tool is an external program that requires separate download.

`transfer_help()` queries the the command line GDC Data Transfer Tool, `gdc-client`, for available options to be used in the `transfer` command.

Usage

```
transfer(manifest, destination_dir = tempfile(), args = character(),
        token = NULL, gdc_client = "gdc-client")
```

```
transfer_help(gdc_client = "gdc-client")
```

Arguments

<code>manifest</code>	character(1) file path to manifest created by <code>manifest()</code> . See write_manifest for a simple way to create a manifest file from a data.frame created with <code>manifest</code> .
<code>destination_dir</code>	The path into which to place the transferred files.
<code>args</code>	character() vector specifying command-line arguments to be passed to <code>gdc-client</code> . See transfer_help for possible values. The arguments <code>--manifest</code> , <code>--dir</code> , and <code>--token-file</code> are determined by <code>manifest</code> , <code>destination_dir</code> , and <code>token</code> , respectively, and should NOT be provided as elements of <code>args</code> .
<code>token</code>	character(1) containing security token allowing access to restricted data. See https://gdc-docs.nci.nih.gov/API/Users_Guide/Authentication_and_Authorization/ . Note that the GDC transfer tool requires a file for data transfer. Therefore, this token will be written to a temporary file (with appropriate permissions set).
<code>gdc_client</code>	character(1) name or path to <code>gdc-client</code> executable. On Windows, use <code>/</code> or <code>\\</code> as the file separator.

Value

character(1) directory path to which the files were downloaded.

Functions

- `transfer_help`:

Examples

```
file_manifest = files() %>% filter(~ access == "open") %>% manifest(size=10)
manifest_file = tempfile()
write.table(file_manifest, file=manifest_file, col.names=TRUE, row.names=FALSE, quote=FALSE)
destination <- transfer(manifest_file)
```

```
dir(destination)
# and with authentication
destination <- transfer(manifest_file, token=gdc_token)
```

write_manifest	<i>write a manifest data.frame to disk</i>
----------------	--

Description

The `manifest` method creates a data.frame that represents the data for a manifest file needed by the GDC Data Transfer Tool. While the file format is nothing special, this is a simple helper function to write a manifest data.frame to disk. It returns the path to which the file is written, so it can be used "in-line" in a call to `transfer`.

Usage

```
write_manifest(manifest, destfile = tempfile())
```

Arguments

manifest	A data.frame with five columns, typically created by a call to <code>manifest</code>
destfile	The filename for saving the manifest.

Value

character(1) the destination file name.

Examples

```
mf = files() %>% manifest(size=10)
write_manifest(mf)
```

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