

Package ‘nhsbsa’

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Title Client for the NHS Business Services Authority Open Data Portal

Version 0.1.0

Description A low-level client for the National Health Service Business Services Authority (NHSBSA) Open Data Portal
<<https://opendata.nhsbsa.net>>, a 'CKAN' data catalogue. Provides thin wrappers around the portal's API actions for listing datasets, retrieving metadata, querying the datastore and downloading resource files. Results are returned as plain data (tibbles and lists) for the caller to interpret.

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URL <https://github.com/rmgpanw/nhsbsa>,
<https://rmgpanw.github.io/nhsbsa/>

BugReports <https://github.com/rmgpanw/nhsbsa/issues>

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nhsbsa-methods	<i>Methods for nhsbsa objects</i>
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Description

Some nhsbsa functions return classed lists with a tailored `print()` method and a `tibble::as_tibble()` method for turning them into a table:

Usage

```
## S3 method for class 'nhsbsa_package'
print(x, ...)

## S3 method for class 'nhsbsa_resource'
print(x, ...)

## S3 method for class 'nhsbsa_package_search'
print(x, ...)

## S3 method for class 'nhsbsa_package'
as_tibble(x, ...)

## S3 method for class 'nhsbsa_package_search'
as_tibble(x, ...)
```

Arguments

- x An object returned by the relevant nhsbsa function.
- ... Ignored, for S3 method consistency.

Details

- `nhsbsa_package_show()` returns an `nhsbsa_package`; `as_tibble()` returns its resources (one row per file). This is the same table as `nhsbsa_list_resources()`, but built from meta-data you have already fetched, so it avoids a second request (and does not filter by pattern).
- `nhsbsa_resource_show()` returns an `nhsbsa_resource`.
- `nhsbsa_package_search()` returns an `nhsbsa_package_search`; `as_tibble()` returns one row per matching dataset.

These objects are still plain lists, so `$`, `[[` and `utils::str()` work as usual. Pass `.return_raw = TRUE` to the originating function, or use `unclass()`, to get the underlying list without a class.

Value

The `print()` methods return `x` invisibly. The `as_tibble()` methods return a [tibble](#).

Examples

```
pkg <- nhsbsa_package_show("english-prescribing-data-epd")
pkg
tibble::as_tibble(pkg)

hits <- nhsbsa_package_search(q = "prescribing", rows = 5)
hits
tibble::as_tibble(hits)
```

`nhsbsa_datastore_search`

Search a resource's rows

Description

Wraps the CKAN `datastore_search` action to read the rows of a datastore resource. One argument is provided for each documented API parameter.

Usage

```
nhsbsa_datastore_search(
  resource_id,
  q = NULL,
  distinct = NULL,
  plain = NULL,
  language = NULL,
  limit = NULL,
  offset = NULL,
  fields = NULL,
  sort = NULL,
  filters = NULL,
```

```

    include_total = NULL,
    .return_raw = FALSE
  )

```

Arguments

resource_id	Character scalar. The resource to query. The NHSBSA datastore identifies a resource by its <i>name</i> (the name column of nhsbsa_list_resources()), e.g. "EPD_201401", rather than its id.
q	A full-text query (a character scalar, or a named list for a per-field search). Accepted for API completeness but not applied by this portal; use nhsbsa_datastore_search_sql() instead.
distinct	Logical. Return only rows that are distinct across the selected fields?
plain	Logical. Controls how a q full-text query is parsed (TRUE, the default, treats q as plain text). Only relevant to q, which this portal does not apply.
language	Character scalar. The text-search language (e.g. "english").
limit	Integer. Maximum number of rows to return in this request.
offset	Integer. Number of rows to skip, for paging.
fields	Character vector. The fields to return, in order.
sort	Character scalar or vector. Sort clause(s), e.g. "ITEMS desc".
filters	Named list. Field-value pairs to filter on. Accepted for API completeness but not applied by this portal; use nhsbsa_datastore_search_sql() instead.
include_total	Logical. Include the total match count in the response? Required for the incomplete-results warning; defaults to the API default (TRUE) when left NULL.
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Details

Use this function to *read* rows — choosing and ordering columns with `fields`, sorting with `sort`, and paging with `limit`/`offset`. To *filter* by value or to aggregate, use [nhsbsa_datastore_search_sql\(\)](#) instead (see Details).

The CKAN datastore returns at most one page of rows per request (the server enforces a maximum `limit`). When more rows exist than are returned, a warning of class `nhsbsa_incomplete_results` is signalled describing how to page through the rest by increasing `offset`.

CKAN's `datastore_search` defines `filters` (exact field matching) and `q` (full-text search) parameters, which this function exposes for API completeness. **This portal's datastore does not apply them** — a query using `filters` or `q` returns no matching rows — so to filter by value, aggregate or compute expressions, use [nhsbsa_datastore_search_sql\(\)](#) with a SQL WHERE/GROUP BY clause. See `vignette("nhsbsa")` for worked examples.

Value

A tibble with one row per record. With `.return_raw = TRUE`, the parsed response envelope as a list (including total and fields).

See Also

[nhsbsa_datastore_search_sql\(\)](#) to filter or aggregate with SQL, [nhsbsa_download_resource\(\)](#) to download the whole resource file.

Examples

```
# Read selected columns, sorted (field names are case-sensitive)
nhsbsa_datastore_search(
  resource_id = "EPD_202401",
  fields = c("PCO_CODE", "BNF_CHEMICAL_SUBSTANCE", "ITEMS"),
  sort = "ITEMS desc",
  limit = 5
)

# Distinct values of a column
nhsbsa_datastore_search(
  resource_id = "EPD_202401",
  fields = "PCO_CODE",
  distinct = TRUE,
  limit = 5
)

# Page through rows with `limit` and `offset`
nhsbsa_datastore_search(resource_id = "EPD_202401", fields = "ITEMS", limit = 5)
nhsbsa_datastore_search(
  resource_id = "EPD_202401",
  fields = "ITEMS",
  limit = 5,
  offset = 5
)

# Use the raw envelope to read the total number of rows
raw <- nhsbsa_datastore_search(
  resource_id = "EPD_202401",
  limit = 1,
  .return_raw = TRUE
)
raw$result$total
```

nhsbsa_datastore_search_sql

Query a resource with SQL

Description

Wraps the CKAN `datastore_search_sql` action, which runs a read-only SQL query against the datastore. The `sql` string is sent to the API verbatim; paging is the caller's responsibility (via `LIMIT/OFFSET` in the query).

Usage

```
nhsbsa_datastore_search_sql(resource_id, sql, .return_raw = FALSE)
```

Arguments

<code>resource_id</code>	Character scalar. The resource the query targets. The NHSBSA datastore requires this alongside <code>sql</code> , and identifies a resource by its <i>name</i> (the name column of <code>nhsbsa_list_resources()</code>), e.g. "EPD_201401". Reference the same name in the query's FROM clause.
<code>sql</code>	Character scalar. A single read-only SQL SELECT statement, e.g. 'SELECT * FROM `EPD_201401` LIMIT 10'.
<code>.return_raw</code>	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A tibble with one row per record returned by the query. With `.return_raw = TRUE`, the parsed response envelope as a list.

See Also

[nhsbsa_datastore_search\(\)](#) for a parameterised search.

Examples

```
# Select specific columns
nhsbsa_datastore_search_sql(
  resource_id = "EPD_202401",
  sql = "SELECT YEAR_MONTH, PCO_CODE, ITEMS FROM `EPD_202401` LIMIT 10"
)

# Filter by value with a WHERE clause (the reliable way to filter)
nhsbsa_datastore_search_sql(
  resource_id = "EPD_202401",
  sql = "SELECT PCO_CODE, BNF_CHEMICAL_SUBSTANCE, ITEMS
        FROM `EPD_202401`
        WHERE PCO_CODE = 'W2U3Z'
        LIMIT 10"
)

# Aggregate server-side: total items prescribed per organisation
nhsbsa_datastore_search_sql(
  resource_id = "EPD_202401",
  sql = "SELECT PCO_CODE, SUM(ITEMS) AS items
        FROM `EPD_202401`
        GROUP BY PCO_CODE
        ORDER BY items DESC
        LIMIT 10"
)
```

`nhsbsa_download_resource`*Download a resource file*

Description

Resolves a single resource within a dataset and streams its file to disk. This is the file-download counterpart to the datastore row-query functions ([nhsbsa_datastore_search\(\)](#) and friends): it fetches the whole resource file (e.g. a CSV) rather than running a query.

Usage

```
nhsbsa_download_resource(  
  dataset_id,  
  directory,  
  resource_id = NULL,  
  pattern = NULL,  
  overwrite = FALSE,  
  quiet = FALSE  
)
```

Arguments

<code>dataset_id</code>	Character scalar. The dataset identifier, as returned by nhsbsa_package_list() .
<code>directory</code>	Character scalar. The directory to download into. Required; there is no default, and the directory must already exist. Use tempdir() for a throwaway location.
<code>resource_id</code>	Character scalar. The identifier of the resource to download. Takes precedence over <code>pattern</code> .
<code>pattern</code>	Character scalar. A regular expression matched (case-insensitively) against resource names to select a single resource.
<code>overwrite</code>	Logical. Overwrite the file if it already exists in <code>directory</code> ? Defaults to <code>FALSE</code> , in which case the existing file is left untouched and its path returned.
<code>quiet</code>	Logical. Suppress informational messages? Defaults to <code>FALSE</code> .

Details

Exactly one resource must be identified. Supply either `resource_id` or a `pattern` that matches a single resource name; if neither is given and the dataset has more than one resource, an error is raised.

The file is saved into `directory` under its own name (the file name from the resource's download URL, e.g. `bnf_code_current_202503_version_88.csv`).

Value

The path to the downloaded file, invisibly.

See Also

[nhsbsa_list_resources\(\)](#) to discover resources.

Examples

```
resources <- nhsbsa_list_resources("bnf-code-information-current-year")

# Identify a resource by a pattern matching a single resource name
path <- nhsbsa_download_resource(
  "bnf-code-information-current-year",
  pattern = resources$name[[1]],
  directory = tempdir()
)
path

# ...or by its exact id. An existing file is not re-downloaded unless
# `overwrite = TRUE`, so this call short-circuits and returns the path.
nhsbsa_download_resource(
  "bnf-code-information-current-year",
  resource_id = resources$id[[1]],
  directory = tempdir()
)
```

nhsbsa_group_list	<i>List dataset groups</i>
-------------------	----------------------------

Description

Wraps the CKAN group_list action to list the groups (thematic collections) that datasets can belong to.

Usage

```
nhsbsa_group_list(all_fields = NULL, .return_raw = FALSE)
```

Arguments

all_fields	Logical. If TRUE, return a richer record for each organisation rather than just its name. Defaults to the API default (FALSE) when left NULL.
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A character vector of group names. If all_fields = TRUE, a list of group records. With .return_raw = TRUE, the parsed response envelope as a list.

See Also

[nhsbsa_organization_list\(\)](#), [nhsbsa_tag_list\(\)](#).

Examples

```
nhsbsa_group_list()
```

`nhsbsa_list_resources` *List a dataset's resources as a tibble*

Description

A convenience wrapper around [nhsbsa_package_show\(\)](#) that returns a dataset's resources as a tibble, optionally filtered by a pattern matched against the resource name. This is the most direct way to discover the resources (and their download URLs) available for a dataset.

Usage

```
nhsbsa_list_resources(dataset_id, pattern = NULL)
```

Arguments

<code>dataset_id</code>	Character scalar. The dataset identifier, as returned by nhsbsa_package_list() .
<code>pattern</code>	Character scalar. An optional regular expression; only resources whose name matches (case-insensitively) are returned.

Details

If you have already fetched the dataset metadata with [nhsbsa_package_show\(\)](#), calling `tibble::as_tibble()` on it gives the same table without a second request (but without the pattern filter).

Value

A tibble with one row per resource and columns `name`, `id`, `format`, `created`, `last_modified`, `url` and `size`.

See Also

[nhsbsa_download_resource\(\)](#) to download a resource file; [nhsbsa_package_show\(\)](#) (with `tibble::as_tibble()`) for the same table from already-fetched metadata.

Examples

```
# All resources for a dataset
nhsbsa_list_resources("english-prescribing-data-epd")

# Only resources whose name matches a pattern
nhsbsa_list_resources("english-prescribing-data-epd", pattern = "202401")
```

`nhsbsa_organization_list`*List publishing organisations*

Description

Wraps the CKAN `organization_list` action to list the organisations that publish datasets on the portal.

Usage

```
nhsbsa_organization_list(all_fields = NULL, .return_raw = FALSE)
```

Arguments

<code>all_fields</code>	Logical. If TRUE, return a richer record for each organisation rather than just its name. Defaults to the API default (FALSE) when left NULL.
<code>.return_raw</code>	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A character vector of organisation names. If `all_fields = TRUE`, a list of organisation records. With `.return_raw = TRUE`, the parsed response envelope as a list.

See Also

[nhsbsa_group_list\(\)](#), [nhsbsa_tag_list\(\)](#).

Examples

```
# Organisation names
nhsbsa_organization_list()

# Richer records (title, description, dataset count, ...) for each organisation
orgs <- nhsbsa_organization_list(all_fields = TRUE)
orgs[[1]]$title
```

nhsbsa_package_list	<i>List available datasets</i>
---------------------	--------------------------------

Description

Wraps the CKAN package_list action to return the identifiers of every dataset published on the NHSBSA Open Data Portal.

Usage

```
nhsbsa_package_list(.return_raw = FALSE)
```

Arguments

.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.
-------------	---

Value

A character vector of dataset identifiers. With .return_raw = TRUE, the parsed response envelope as a list.

See Also

[nhsbsa_package_show\(\)](#) for a dataset's metadata, [nhsbsa_package_search\(\)](#) to search datasets.

Examples

```
datasets <- nhsbsa_package_list()
length(datasets)
head(datasets)
```

nhsbsa_package_search	<i>Search datasets</i>
-----------------------	------------------------

Description

Wraps the CKAN package_search action, a Solr-backed search over datasets.

Usage

```
nhsbsa_package_search(  
  q = NULL,  
  fq = NULL,  
  sort = NULL,  
  rows = NULL,  
  start = NULL,  
  .return_raw = FALSE  
)
```

Arguments

q	Character scalar. The Solr query string (e.g. "prescribing"). Defaults to NULL (match all).
fq	Character scalar. A Solr filter query.
sort	Character scalar. Sort order, e.g. "metadata_modified desc".
rows	Integer. Maximum number of datasets to return.
start	Integer. Offset into the result set, for paging.
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A list with the search count and matching datasets in `results`, with class `nhsbsa_package_search` and a `print()` method; `tibble::as_tibble()` turns the results into one row per dataset. With `.return_raw = TRUE`, the parsed response envelope as a plain list.

Examples

```
# Free-text search  
hits <- nhsbsa_package_search(q = "prescribing", rows = 5)  
hits  
tibble::as_tibble(hits)  
  
# Filter by tag (as clicking a tag on the website does) and sort the results  
nhsbsa_package_search(  
  fq = 'tags:"Prescribing"',  
  sort = "metadata_modified desc",  
  rows = 5  
)  
  
# Page through results with `rows` and `start`  
nhsbsa_package_search(q = "dental", rows = 10, start = 10)
```

nhsbsa_package_show	<i>Show a dataset's metadata</i>
---------------------	----------------------------------

Description

Wraps the CKAN package_show action to return the full metadata for a single dataset, including its list of resources (downloadable files and datastore tables).

Usage

```
nhsbsa_package_show(id, .return_raw = FALSE)
```

Arguments

id	Character scalar. The dataset identifier or name, as returned by nhsbsa_package_list() .
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A list of dataset metadata, with class `nhsbsa_package` and a [print\(\)](#) method; [tibble::as_tibble\(\)](#) turns it into a table of its resources. With `.return_raw = TRUE`, the parsed response envelope as a plain list.

See Also

[nhsbsa_list_resources\(\)](#) for a tidy table of a dataset's resources.

Examples

```
metadata <- nhsbsa_package_show("english-prescribing-data-epd")
metadata
metadata$title

# The dataset's resources as a tibble
tibble::as_tibble(metadata)
```

nhsbsa_resource_show	<i>Show a resource's metadata</i>
----------------------	-----------------------------------

Description

Wraps the CKAN resource_show action to return the metadata for a single resource (a file or datastore table).

Usage

```
nhsbsa_resource_show(id, .return_raw = FALSE)
```

Arguments

id	Character scalar. The resource identifier.
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A list of resource metadata, with class nhsbsa_resource and a [print\(\)](#) method. With .return_raw = TRUE, the parsed response envelope as a plain list.

Examples

```
resources <- nhsbsa_list_resources("english-prescribing-data-epd")
meta <- nhsbsa_resource_show(resources$id[[1]])
meta$name
meta$datastore_active
```

nhsbsa_tag_list	<i>List tags</i>
-----------------	------------------

Description

Wraps the CKAN tag_list action to list the tags applied to datasets. These are the same tags shown on the portal website; you can filter datasets by a tag with [nhsbsa_package_search\(\)](#) (see [vignette\("nhsbsa"\)](#)).

Usage

```
nhsbsa_tag_list(query = NULL, vocabulary_id = NULL, .return_raw = FALSE)
```

Arguments

query	Character scalar. Restrict the results to tags containing this string.
vocabulary_id	Character scalar. Restrict the results to tags in a particular CKAN tag vocabulary.
.return_raw	Logical. If TRUE, return the full parsed CKAN response envelope instead of the processed result. Defaults to FALSE.

Value

A character vector of tags. With `.return_raw = TRUE`, the parsed response envelope as a list.

See Also

[nhsbsa_package_search\(\)](#) to find datasets by tag.

Examples

```
# All tags
tags <- nhsbsa_tag_list()
length(tags)

# Only tags containing a given string
nhsbsa_tag_list(query = "prescribing")
```

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