

Package: standartox (via r-universe)

October 19, 2026

Version 1.0.0

Date 2025-09-19

Title Ecotoxicological Information from the Standartox Database

Maintainer Andreas Scharmüller <andschar@protonmail.com>

Description The Standartox database offers cleaned, harmonized and aggregated ecotoxicological test data, which can be used for assessing effects and risks of chemical concentrations found in the environment.

Depends R (>= 3.5.0)

Imports stats, httr (>= 1.4.1), curl (>= 3.4), jsonlite (>= 1.6.1),
fst (>= 0.9.4), data.table (>= 1.17.8)

License MIT + file LICENSE

URL <https://github.com/andschar/standartox>

BugReports <https://github.com/andschar/standartox/issues>

RoxygenNote 7.3.2

Encoding UTF-8

Config/pak/sysreqs libssl-dev

Repository <https://andschar.r-universe.dev>

Date/Publication 2025-09-24 11:02:03 UTC

RemoteUrl <https://github.com/andschar/standartox>

RemoteRef HEAD

RemoteSha a5561d3cc1325dd432ae70c71fbbda40f047423a

Contents

stx_catalog	2
stx_chem	3
stx_data	4
stx_meta	5
stx_query	6
stx_taxa	9

Index**11**

stx_catalog

Retrieve Standartox Data Catalog

Description

Retrieves a catalog of all possible values for variables that can be used for filtering in `stx_query()`. This is useful for discovering valid inputs for parameters like `endpoint_group`, `effect`, or `tax_group`.

Usage

```
stx_catalog(silent = FALSE, stx_dir = file.path(tempdir(), "standartox"))
```

Arguments

<code>silent</code>	logical; If TRUE, suppresses messages during the download process. Default is FALSE.
<code>stx_dir</code>	character; Directory where the catalog file is stored. If the file doesn't exist, it will be downloaded to this location. Defaults to a "standartox" subdirectory within the session's temporary directory (<code>tempdir()</code>).

Value

Returns a list where each element is a character vector containing the unique values for a specific data field available for querying.

Author(s)

Andreas Scharm Mueller <andschar@protonmail.com>
Hannes Reinwald

Examples

```
# This function might fail if there is no internet connection or Zenodo.org is not available

# Basic function call to retrieve the catalog
catalog_data <- stx_catalog()

# View the names of available fields in the catalog
names(catalog_data)

# See all possible values for 'endpoint_group'
print(catalog_data$endpoint_group)

# Get verbose output from the function
catalog_verbose <- stx_catalog(silent = FALSE)

# Specify a permanent directory to download and cache the catalog file.
```

```
# This speeds up future calls as the file won't need to be re-downloaded when starting a new session.
my_dir <- file.path("~", "my_stx_data")
catalog_cached <- stx_catalog(stx_dir = my_dir, silent = FALSE)
```

stx_chem

Retrieve the Standartox Chemical Properties Table

Description

Provides direct access to the 'phch' data table, which contains chemical identifiers and physico-chemical properties for all compounds in the Standartox database.

Usage

```
stx_chem(silent = FALSE, stx_dir = file.path(tempdir(), "standartox"))
```

Arguments

silent	logical; If 'TRUE', suppresses progress messages during download. Defaults to 'FALSE'.
stx_dir	character; Directory where the chemical data file is stored or should be downloaded. Defaults to a "standartox" subdirectory within the session's temporary directory (file.path(tempdir(), "standartox")).

Details

This function is a simple wrapper for `stx_download(data_type = 'phch')`. It is designed for users who want to explore the chemical inventory of the database, for instance, to find CAS numbers for use with [stx_query](#).

Like other download functions in this package, it caches the data file locally to avoid re-downloading on subsequent calls.

Value

A `data.table` containing chemical information, including columns such as CAS number, chemical name, and other identifiers.

Author(s)

Andreas Scharm Mueller <andschar@protonmail.com>

Hannes Reinwald

Examples

```
# This function may fail if there is no internet connection or Zenodo.org is not available

# Basic function call to retrieve the chemical data table
chem_data <- stx_chem()

# Inspect the first few rows and column names to see what's available
head(chem_data)
colnames(chem_data)

# Example of using a permanent directory to cache the data file
# The "Retrieving..." message will only appear on the first download.
my_dir <- file.path("~", "my_stx_data")
cached_chem_data <- stx_chem(stx_dir = my_dir, silent = FALSE)
```

stx_data

Retrieve the Core Standartox Toxicity Data Table

Description

Provides direct access to the main ‘test_fin’ data table from the Standartox database, which contains the raw toxicity results.

Usage

```
stx_data(silent = FALSE, stx_dir = file.path(tempdir(), "standartox"))
```

Arguments

silent	logical; If ‘TRUE’, suppresses progress messages during download. Defaults to ‘FALSE’.
stx_dir	character; Directory where the data file is stored or should be downloaded. Defaults to a "standartox" subdirectory within the session’s temporary directory (file.path(tempdir(), "standartox")).

Details

This function is a simple wrapper for `stx_download(data_type = 'test_fin')`. It is designed for users who want the primary data table of toxicity test results without the additional chemical or detailed taxonomic information that [stx_query](#) automatically appends.

Like other download functions in this package, it caches the data file locally to avoid re-downloading on subsequent calls.

Value

A data.table containing the core toxicity test results, with columns for endpoints, duration, concentration, effect, etc.

Author(s)

Andreas Scharm Mueller <andschar@protonmail.com>

Hannes Reinwald

Examples

```
# This function may fail if there is no internet connection or Zenodo.org is not available

# Basic function call to retrieve the main data table
tox_data <- stx_data()

# Inspect the first few rows and column names to understand the structure
head(tox_data)
colnames(tox_data)

# Example of using a permanent directory to cache the data
# The message "Retrieving Standartox data.." will only appear on the first download.
my_dir <- file.path("~", "my_stx_data")
cached_data <- stx_data(stx_dir = my_dir, silent = FALSE)
```

stx_meta

Retrieve meta data

Description

Retrieve meta data

Usage

```
stx_meta(silent = FALSE, stx_dir = file.path(tempdir(), "standartox"))
```

Arguments

silent	logical; If TRUE, suppresses messages. Default is FALSE.
stx_dir	character; Directory to which the meta information should be downloaded. Default is a temporary directory.#'

Value

Returns a data.table containing meta information on Standartox.

Author(s)

Andreas Scharm Mueller <andschar@protonmail.com>

Hannes Reinwald

Examples

```
# might fail if there is no internet connection or Zenodo.org not available
# basic function call
df = stx_meta()

# to get verbose output from the function
df = stx_meta(silent = FALSE)

# to specify a directory to which the taxa information should be downloaded
df = stx_meta(silent = FALSE, stx_dir = "~/tmp")
# This will create a directory under ~/tmp and download the respective standartox file to that directory.
# The files are then permanently stored in that directory and can be directly read when restarting your R session.
```

stx_query

Query and Filter Standartox Toxicity Data

Description

Retrieves and filters toxicity data from the Standartox database (<https://doi.org/10.5281/zenodo.3785030>). This function acts as a powerful front-end for subsetting the database based on chemical, experimental, and taxonomic criteria.

Usage

```
stx_query(
  cas_number = NULL,
  endpoint_group = c("XX50", "NOEX", "LOEX"),
  endpoint_qualifier = "=",
  endpoint = NULL,
  exposure = NULL,
  effect = NULL,
  measurement = NULL,
  duration = c(0, Inf),
  duration_unit = "h",
  concentration_unit = NULL,
  concentration_type = NULL,
  organism_lifestage = NULL,
  tax_columns = c("tax_group", "tax_taxon", "tax_genus", "tax_family"),
  tax_genus = NULL,
  tax_family = NULL,
  tax_order = NULL,
  tax_class = NULL,
  tax_group = NULL,
  include_reference = FALSE,
  rm_NR = TRUE,
```

```

    verbose = FALSE,
    ...
)

```

Arguments

cas_number	character; Optional vector of CAS numbers to filter by (e.g., <code>c("1071-83-6", "63-25-2")</code>). If 'NULL' (default), results for all chemicals are returned.
endpoint_group	character; Optional vector of endpoint groups to filter results. See <code>stx_catalog()\$endpoint_group</code> for all possible values. Defaults to <code>c("XX50", "NOEX", "LOEX")</code> .
endpoint_qualifier	character; Optional vector of endpoint value qualifiers (e.g., <code>c(">", "<=")</code>). Common values are "=", ">", "<", "~", "<=", ">=". Defaults to "=" . Set to 'NULL' to include all qualifiers.
endpoint	character; Optional vector of specific endpoints to filter by (e.g., "LC50", "NOEC"). If 'NULL' (default), no endpoint filtering is applied.
exposure	character; Optional vector of exposure types. See <code>stx_catalog()\$exposure</code> . If 'NULL' (default), no exposure type filtering is applied.
effect	character; Optional vector of observed effects. See <code>stx_catalog()\$effect</code> . If 'NULL' (default), no effect filtering is applied.
measurement	character; Optional vector of measurement types. See <code>stx_catalog()\$measurement</code> . If 'NULL' (default), no measurement filtering is applied.
duration	numeric; A numeric vector of length two specifying the duration range (in hours) to filter by, e.g., <code>c(24, 96)</code> . Defaults to <code>c(0, Inf)</code> , including all durations.
duration_unit	character; Filter by the unit of duration. See <code>stx_catalog()\$duration_unit</code> . Defaults to "h" (hours). Set to 'NULL' to keep all units.
concentration_unit	character; Optional vector of concentration units. See <code>stx_catalog()\$concentration_unit</code> . If 'NULL' (default), no filtering is applied.
concentration_type	character; Optional vector of concentration types. See <code>stx_catalog()\$concentration_type</code> . If 'NULL' (default), no filtering is applied.
organism_lifestage	character; Optional vector of organism lifestages. See <code>stx_catalog()\$organism_lifestage</code> . If 'NULL' (default), no lifestage filtering is applied.
tax_columns	character; A vector of taxonomic column names to append to the results. See <code>colnames(stx_taxa())</code> for all options. Defaults to <code>c("tax_group", "tax_taxon", "tax_genus", "tax_family")</code> .
tax_genus	character; Optional vector of genera to filter by. See <code>stx_catalog()\$genus</code> . If 'NULL' (default), no genus filtering is applied.
tax_family	character; Optional vector of families to filter by. See <code>stx_catalog()\$family</code> . If 'NULL' (default), no family filtering is applied.
tax_order	character; Optional vector of orders to filter by. See <code>stx_catalog()\$order</code> . If 'NULL' (default), no order filtering is applied.

tax_class	character; Optional vector of classes to filter by. See <code>stx_catalog()\$class</code> . If 'NULL' (default), no class filtering is applied.
tax_group	character; Optional vector of ecotoxicological groups to filter by. See <code>stx_catalog()\$tax_group</code> for valid inputs (e.g., "invertebrate", "fish"). If 'NULL' (default), no group filtering is applied.
include_reference	logical; If 'TRUE', reference information (author, year, title) is appended to the results. Defaults to FALSE.
rm_NR	logical; If 'TRUE' (default), rows with "NR" (not reported) values in the critical 'endpoint' and 'duration_unit' columns are removed early in the query process. Note that at the end of the query, all remaining "NR" values in any character column are converted to 'NA'.
verbose	logical; If 'TRUE', prints messages detailing the query progress. Defaults to FALSE.
...	Additional arguments to be passed on to stx_download , such as 'stx_dir' to specify a cache directory.

Details

The function operates in a sequential process: 1. It first downloads the necessary data tables ('test_fin', 'phch', 'taxa', and optionally 'refs') using [stx_download](#). 2. It performs initial, fast filtering based on 'endpoint_group', 'endpoint_qualifier', and 'duration_unit'. 3. It then appends chemical and taxonomic information, filtering by 'cas_number' and the 'tax_*' parameters. 4. Finally, it applies the remaining experimental filters ('effect', 'duration', 'concentration_unit', etc.).

By default, filters are combined with a logical "AND". For example, specifying a 'tax_genus' and an 'effect' will return only records that match both criteria.

'stx_catalog()' is a helper function that provides a list of all valid filter values for many of this function's parameters.

Value

A data.table containing the filtered Standartox toxicity data. If the query results in zero matches, the function returns 'NULL' and issues a warning.

Author(s)

Hannes Reinwald

Examples

```
# This function may fail if there is no internet connection or Zenodo.org is not available

# Basic query using default filters (XX50, NOEX, LOEX endpoints in hours)
# Using verbose=TRUE to see the process
results_default <- stx_query(verbose = TRUE)

# To see available filter options, use the catalog function
catalog <- stx_catalog()
```

```

print(catalog$endpoint_group)

# Query for a specific CAS number and multiple specific endpoints for key taxonomic groups
q1 <- stx_query(
  cas_number = "1071-83-6", # Glyphosate
  endpoint = c("LC50", "EC50", "LOEC", "NOEC"),
  duration = c(0, 120), # Up to 120 hours
  tax_group = c("invertebrate", "fish", "algae")
)

# Get all >LC50 values for Zebra fish (Danio rerio) embryos or larvae,
# including reference information
q2 <- stx_query(
  endpoint = "LC50",
  endpoint_qualifier = ">",
  duration = c(72, 120),
  tax_genus = "Danio",
  organism_lifestage = c("Embryo", "Larva"),
  include_reference = TRUE,
  verbose = TRUE
)

# Get all XX50 acute toxicity values for the family Daphniidae related to mobility
q3 <- stx_query(
  endpoint_group = "XX50",
  duration = c(24, 48),
  measurement = c("immobile", "mobility", "swimming"),
  tax_family = "Daphniidae",
  include_reference = TRUE
)

```

stx_taxa

Retrieve the Standartox Taxonomy Table

Description

Provides direct access to the ‘taxa’ data table, which contains the complete taxonomic classification for every species in the Standartox database.

Usage

```
stx_taxa(silent = FALSE, stx_dir = file.path(tempdir(), "standartox"))
```

Arguments

silent	logical; If ‘TRUE’, suppresses progress messages during download. Defaults to ‘FALSE’.
--------	--

stx_dir character; Directory where the taxonomy data file is stored or should be downloaded. Defaults to a "standartox" subdirectory within the session's temporary directory (`file.path(tempdir(), "standartox")`).

Details

This function is a simple wrapper for `stx_download(data_type = 'taxa')`. It is designed for users who want to explore the full taxonomic scope of the database or find valid inputs for the 'tax_genus', 'tax_family', and 'tax_group' parameters in [stx_query](#).

Like other download functions in this package, it caches the data file locally to avoid re-downloading on subsequent calls.

Value

A data.table containing taxonomic classifications, with columns such as 'tax_genus', 'tax_family', 'tax_order', and 'tax_group'.

Author(s)

Andreas Scharm Mueller <andschar@protonmail.com>

Hannes Reinwald

Examples

```
# This function may fail if there is no internet connection or Zenodo.org is not available

# Basic function call to retrieve the taxonomy data table
taxa_data <- stx_taxa()

# Inspect the first few rows and see all available columns
head(taxa_data)
colnames(taxa_data)

# Find all unique ecotoxicological groups in the database
if (nrow(taxa_data) > 0) {
  print(unique(taxa_data$tax_group))
}

# Example of using a permanent directory to cache the data file
my_dir <- file.path("~", "my_stx_data")
cached_taxa_data <- stx_taxa(stx_dir = my_dir, silent = FALSE)
```

Index

stx_catalog, [2](#)
stx_chem, [3](#)
stx_data, [4](#)
stx_download, [8](#)
stx_meta, [5](#)
stx_query, [3](#), [4](#), [6](#), [10](#)
stx_taxa, [9](#)