

toxvaldbmain

September 5, 2024

Type Package

Title Builds the ToxValDB V9.5 Database

Version 9.5

Author Taylor Wall

Maintainer Taylor Wall <wall.taylor@epa.gov>

Description

ToxValDB is a database containing quantitative records from in vivo toxicology studies from many sources. The database has 2 main parts - toxval_source containing source data in separate tables, and the main toxval schema which combines data from multiple sources into a single format. This project moves data from toxval_source to toxval. Data is read from files or other databases into toxval_source and then pulled into toxval where terms are converted to standard values. The ToxValDB SOPs describe in more detail how to run the code. This version is setup to build ToxValDB v9.5

Imports DBI,
RMySQL,
openxlsx,
dplyr,
tidyr,
stringr,
tibble,
janitor,
XML,
miniUI,
RCurl,
gsubfn,
textclean,
magrittr

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Contents

cas_checkSum	5
check.toxval_type.route.units	6
chem.check.v2	7
clean.last.character	7
clean.toxval.by.source	8
compare.versions	9
duplicate.hunter	9
ecotox.select.study.duration	10
ecotox.select.toxval.numeric	10
ecotox.species.dictionary	11
export.all.by.source	11
export.for.missing.species	12
export.for.oppt	12
export.for.toxval.qc	13
export.for.toxvaldb.manuscript	13
export.missing.dictionary.entries	14
export.missing.strains	14
export.missing.toxval_type	15
export.toxvaldb.subset	15
export.update.source.info	16
fill.chemical.by.source	16
fill.toxval.defaults	17
fill.toxval.defaults.global.by.source	17
fix.all.param.by.source	18
fix.associated.pod.critical_effect	18
fix.casrn	19
fix.critical_effect.icf.by.source	20
fix.dedup.hierarchy.by.source	20
fix.derived.toxval_type.by.source	21
fix.empty.by.source	22
fix.empty.record_source.by.source	22
fix.exposure.params	23
fix.generation.by.source	23
fix.human_eco.by.source	24
fix.non_ascii.v2	24
fix.priority_id.by.source	25
fix.qc_status.by.source	26
fix.replace.unicode	26
fix.risk_assessment_class.by.source	27
fix.single.param.by.source	28
fix.species.common_name	28

fix.species.duplicates	29
fix.species.v2	29
fix.strain.v2	30
fix.study_duration.params	30
fix.study_group	31
fix.study_type.by.source	32
fix.trim_spaces	33
fix.units.by.source	33
generate originals	34
getDBConn	35
import.dictionary	35
import.source.info.by.source	36
load.dsstox	36
log_message	37
printCurrentFunction	37
pull_jira_info	38
qa_toxval_url_validation	39
runInsert	40
runInsertTable	41
runQuery	42
runStatement	43
runUpdate	44
set.critical_effect_category	45
set.experimental_record.by.source	45
set.initial.qc_status	46
set.qc.category.by.source	46
set.study_type.by.study_group	47
set.supersource.export.names	48
set_extraction_doc_clowder_id	48
set_toxval_relationship_by_toxval_type	49
source_chemical.chemidplus	49
source_chemical.ecotox	50
source_chemical.extra	51
source_chemical.toxrefdb	51
source_hash_vectorized	52
species.qc	53
species.strain.mismatch	53
toxval.config	54
toxval.init.db	55
toxval.load.alaska_dec	55
toxval.load.all	56
toxval.load.atsdr.pfas.2021	57
toxval.load.atsdr.mrls	57
toxval.load.caloezza	58
toxval.load.cancer	58
toxval.load.chemidplus	59
toxval.load.copper	60
toxval.load.dedup	60

toxval.load.dod	61
toxval.load.doe.benchmarks	62
toxval.load.doe.pac	62
toxval.load.echa_iuclid	63
toxval.load.ecotox	64
toxval.load.efsa	64
toxval.load.epa_aegl	65
toxval.load.epa_hhtv	65
toxval.load.epa_ow_npdwr	66
toxval.load.epa_ow_nrwqc_hhc	66
toxval.load.generic	67
toxval.load.genetox.all	68
toxval.load.gestis.dnel	68
toxval.load.hawc	69
toxval.load.hawc_pfas_150	69
toxval.load.hawc_pfas_430	70
toxval.load.healthcanada	70
toxval.load.heatst	71
toxval.load.hess	72
toxval.load.hpvis	72
toxval.load.initial	73
toxval.load.iris	73
toxval.load.mass_mmcl	74
toxval.load.niosh	74
toxval.load.ntp.pfas	75
toxval.load.opp	75
toxval.load.osha_air_limits	76
toxval.load.ow_dwsha	76
toxval.load.penn	77
toxval.load.penn_dep_mscs	77
toxval.load.pfas_150_sem_v2	78
toxval.load.postprocess	78
toxval.load.pprtv.cphea	79
toxval.load.rsl	80
toxval.load.skin.eye	80
toxval.load.source_chemical	81
toxval.load.species	81
toxval.load.test	82
toxval.load.toxrefdb2.1	82
toxval.load.usgs_hbsl	83
toxval.load.ut_hb	83
toxval.load.who_ipcs	84
toxval.load.who_jecfa_adi	84
toxval.load.who_jecfa_tox_studies	85
toxval.set.mw	85
toxval.summary.stats	86
toxvaldb.view	86
toxval_type.species.mismatch	87

<code>cas_checkSum</code>	5
---------------------------	---

<code>%>%</code>	87
-------------------------------	----

Index	88
--------------	-----------

<code>cas_checkSum</code>	<code>cas_checkSum</code>
---------------------------	---------------------------

Description

Check CAS RN validity via checksum method
For a suspected CAS RN, determine validity by calculating final digit checksum

Usage

```
cas_checkSum(x, checkLEN = TRUE)
```

Arguments

- `x` chr. Input vector of values to check. Standard CAS notation using hyphens is fine, as `#` all non-digit characters are stripped for checksum calculation. Each element of `x` should contain `#` only one suspected CAS RN to check.
- `checkLEN` logi. Should the function check that the non-digit characters of `x` are at least 4, but no `#` more than 10 digits long? Defaults to TRUE. `#`

Details

This function performs a very specific type of check for CAS validity, namely whether the final digit checksum follows the CAS standard. By default, it also ensures that the digit length is compatible with CAS standards. It does nothing more.
This means that there is no check for valid CAS format. Use the `cas_detect` function to check CAS format beforehand, or write your own function if necessary.

Value

A logical vector of length `x` denoting whether each `x` is a valid CAS by the checksum method. NA input values will remain NA.

Note

This is a vectorized, reasonably high-performance version of the `is.cas` function found in the `webchem` package. The functionality encompasses only the actual checksum checking of `webchem::is.cas`; as mentioned in details, use `cas_detect` to recreate the CAS format + checksum checking in `webchem::is.cas`. See examples.
Short of looking up against the CAS registry, there is no way to be absolutely sure that even inputs that pass the checksum test are actually registered CAS RNs. The short digit length of CAS IDs combined with the modulo 10 single- digit checksum means that even within a set of randomly generated validly-formatted CAS entities, ~10% will pass checksum.

See Also

[str_detect](#), [str_pad](#)

Examples

```
cas_good <- c("71-43-2", "18323-44-9", "7732-18-5") #benzene, clindamycin, water
cas_bad  <- c("61-43-2", "18323-40-9", "7732-18-4") #single digit change from good
cas_checkSum(c(cas_good, cas_bad))
```

check.toxval_type.route.units
<i>Output distinct combinations of toxval_type, exposure_route, and toxval_units to check</i>

Description

Output distinct combinations of toxval_type, exposure_route, and toxval_units to check

Usage

```
check.toxval_type.route.units(
  toxval.db,
  source = NULL,
  subsource = NULL,
  load.dict = "Repo/dictionary/toxval_type.route.units.dictionary.xlsx"
)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	Source to check
subsource	Subsource to check (NULL default)
load.dict	Name of dictionary containing expected combinations, or NULL if dictionary should not be read

chem.check.v2	<i>Check the chemicals from a file Names with special characters are cleaned and trimmed CASRN are fixed (dashes put in, trimmed) and check sums are calculated The output is sent to a file called chem-check.xlsx in the source data file One option for using this is to edit the source file until no errors are found</i>
---------------	--

Description

Check the chemicals from a file Names with special characters are cleaned and trimmed CASRN are fixed (dashes put in, trimmed) and check sums are calculated The output is sent to a file called chemcheck.xlsx in the source data file One option for using this is to edit the source file until no errors are found

Usage

```
chem.check.v2(res0, in_source = NULL, verbose = FALSE)
```

Arguments

res0	The data frame in which chemicals names and CASRN will be replaced
in_source	The source to be processed. If source=NULL, process all sources
verbose	If TRUE, print diagnostic messages

Value

Return a list with fixed CASRN and name and flags indicating if fixes were made: res0=res0,name.OK=name.OK,casrn.OK=casrn.OK

clean.last.character	<i>clean.last.character</i>
----------------------	-----------------------------

Description

Clean unneeded characters from the end of a string

Usage

```
clean.last.character(x)
```

Arguments

x	String to be cleaned
---	----------------------

Details

DETAILS

Value

The cleaned string

See Also

[str_trim](#)

Examples

```
## Not run:  
if(interactive()){  
  #EXAMPLE1  
}  
  
## End(Not run)
```

clean.toxval.by.source

Delete a portion of the contents of the toxval database

Description

Delete a portion of the contents of the toxval database

Usage

```
clean.toxval.by.source(toxval.db, source)
```

Arguments

toxval.db	The version of toxval from which the data is deleted.
source	The data source name

Value

The database will be altered

compare.versions	<i>Compare versions of toxval</i>
------------------	-----------------------------------

Description

Compare versions of toxval

Usage

```
compare.versions(db1, db2)
```

Arguments

db1	The old version of the database
db2	The new version of the database

duplicate.hunter	<i>Diagnose duplicates</i>
------------------	----------------------------

Description

Diagnose duplicates

Usage

```
duplicate.hunter(toxval.db, source = NULL, source_table = NULL)
```

Arguments

toxval.db	Database version
source	The source to be updated

Value

Write a file with the results

```
ecotox.select.study.duration
```

ECOTOX Select study_duration

Description

Function to select the appropriate study_duration value from conc1_* fields

Usage

```
ecotox.select.study.duration(in_data)
```

Arguments

in_data	Input ECOTOX dataframe
---------	------------------------

Value

Processed dataframe with new study_duration_values, units, and qualitiifer fields

```
ecotox.select.toxval.numeric
```

ECOTOX Select toxval_numeric

Description

Function to select the appropriate toxval_numeric value from conc1_* fields

Usage

```
ecotox.select.toxval.numeric(in_data)
```

Arguments

in_data	Input ECOTOX dataframe
---------	------------------------

Value

Processed dataframe with new toxval_numeric, units, and qualitiifer fields

`ecotox.species.dictionary`*Extract the ECOTOX species dictionary from the ECOTOX data*

Description

Extract the ECOTOX species dictionary from the ECOTOX data

Usage

```
ecotox.species.dictionary(toxval.db, do.load = F, sys.date = "2023-05-03")
```

Arguments

<code>toxval.db</code>	The version of toxval into which the tables are loaded.
<code>do.load</code>	If TRUE, load the data from the input file and put into a global variable
<code>source.db</code>	The version of toxval source - used to manage chemicals
<code>verbose</code>	Whether the loaded rows should be printed to the console.
<code>log</code>	If TRUE, send output to a log file

<code>export.all.by.source</code>	<i>Build a data frame of the data from toxval and export by source as a series of xlsx files</i>
-----------------------------------	--

Description

Build a data frame of the data from toxval and export by source as a series of xlsx files

Usage

```
export.all.by.source(toxval.db, source = NULL, subsource = NULL)
```

Arguments

<code>toxval.db</code>	Database version
<code>source</code>	The source to be updated
<code>subsource</code>	The subsource to be updated #' @return for each source writes an Excel file with the name ../export/export_by_source_data/toxval_all_toxval.db_source.xlsx

`export.for.missing.species`*Export the records with missing species and point of departure values*

Description

Export the records with missing species and point of departure values

Usage

```
export.for.missing.species(toxval.db, source = NULL)
```

Arguments

<code>toxval.db</code>	Database version
<code>source</code>	The source to be updated #' @return for each source writes an Excel file with the name ../export/export_by_source_data/toxval_all_toxval.db_source.xlsx

`export.for.oppt`*Build a data frame of the PODs and exports as xlsx*

Description

Build a data frame of the PODs and exports as xlsx

Usage

```
export.for.oppt(toxval.db, file.name = "TSCA PICS")
```

Arguments

<code>toxval.db</code>	Database version
<code>file.name</code>	If not NA, this is a file containing chemicals, and only those chemicals will be exported

Value

writes an Excel file with the name ../export/toxval_pod_summary_[human_eco]_Sys.Date().xlsx

export.for.toxval.qc *Build a data frame of the PODs and exports as xlsx*

Description

Build a data frame of the PODs and exports as xlsx

Usage

```
export.for.toxval.qc(toxval.db, source = NULL)
```

Arguments

toxval.db	Database version
human_eco	Either 'human health' or 'eco'
file.name	If not NA, this is a file containing chemicals, and only those chemicals will be exported

Value

writes an Excel file with the name ../export/toxval_pod_summary_[human_eco]_Sys.Date().xlsx

export.for.toxvaldb.manuscript
 Build a data frame of the data for the toxval manuscript

Description

Build a data frame of the data for the toxval manuscript

Usage

```
export.for.toxvaldb.manuscript(toxval.db)
```

Arguments

toxval.db	Database version
source	The source to be updated

Value

Write a file with the results

```
export.missing.dictionary.entries
```

Find "original" values that have not been included in the dictionaries and export them

Description

Find "original" values that have not been included in the dictionaries and export them

Usage

```
export.missing.dictionary.entries(
  toxval.db,
  source = NULL,
  subsources = NULL,
  report.only = FALSE
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If source=NULL, fix all sources
subsources	The subsources to be fixed (NULL default)
report.only	Whether to report or write/export data. Default is FALSE (write/export data)

Value

An excel file in dictionaries with the missing entries (if report.only=TRUE, return tibble) "missing dictionary entries Sys.Date.xlsx"

```
export.missing.strains
```

Set the strain information in toxval

Description

Set the strain information in toxval

Usage

```
export.missing.strains(toxval.db, date_string = "2024-02-27")
```

Arguments

toxval.db	The version of the database to use
date_string	The date of the latest dictionary version

`export.missing.toxval_type`*Export any toxval_types that are not in the toxval_type dictionary*

Description

Export any toxval_types that are not in the toxval_type dictionary

Usage

```
export.missing.toxval_type(toxval.db, report.only = FALSE)
```

Arguments

<code>toxval.db</code>	The version of toxval in which the data is altered.
<code>report.only</code>	Whether to report or write/export data. Default is FALSE (write/export data)

Value

An excel file in dictionaries with the missing entries (if report.only=TRUE, return tibble) "dictionary/missing/missing_toxval_type Sys.Date.xlsx"

`export.toxvaldb.subset`*Build a data frame of the data from toxval for a subset of chemicals*

Description

Build a data frame of the data from toxval for a subset of chemicals

Usage

```
export.toxvaldb.subset(toxval.db, filename)
```

Arguments

<code>toxval.db</code>	Database version
<code>filename</code>	The name of the file to be imported - should be a short name that will be used in the output filename. This is an xlsx file and needs a column labeled dtxsid

Value

Write a file with the results

```
export.update.source.info
```

export.update.source.info

Description

Pull updated field information for source info dictionary

Usage

```
export.update.source.info(toxval.db, source.db, dict_date = "2024-08-28")
```

Arguments

toxval.db	Database version
source.db	The source to be updated
dict_date	Date stamp of the dictionary file to update

Value

Overwrite existing source info dictionary with updated fields

```
fill.chemical.by.source
```

Fill the chemical table

Description

Fill the chemical table

Usage

```
fill.chemical.by.source(toxval.db, source, verbose = TRUE)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	The source to be used
verbose	If TRUE, print out extra diagnostic messages

fill.toxval.defaults *Set Toxval Defaults*

Description

Set Toxval Defaults

Usage

```
fill.toxval.defaults(toxval.db, mat)
```

Arguments

toxval.db	The version of toxval from which to set defaults.
mat	An input matrix of data

Value

The data matrix afer fixing

fill.toxval.defaults.global.by.source
Set Toxval Defaults globally, replacing blanks with -

Description

Set Toxval Defaults globally, replacing blanks with -

Usage

```
fill.toxval.defaults.global.by.source(  
  toxval.db,  
  source = NULL,  
  subsource = NULL  
)
```

Arguments

toxval.db	The version of toxval from which to set defaults.
source	The source to be fixed
subsource	The subsource to be fixed (NULL default)

```
fix.all.param.by.source
```

Alter the contents of toxval according to an excel dictionary file with fields - exposure_method, exposure_route, sex, strain, study_duration_class, study_duration_units, study_type, toxval_type, exposure_form, media, toxval_subtype

Description

Alter the contents of toxval according to an excel dictionary file with fields - exposure_method, exposure_route, sex, strain, study_duration_class, study_duration_units, study_type, toxval_type, exposure_form, media, toxval_subtype

Usage

```
fix.all.param.by.source(  
  toxval.db,  
  source = NULL,  
  subsources = NULL,  
  fill.toxval_fix = TRUE  
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If source=NULL, fix all sources
subsources	The subsources to be fixed (NULL default)
fill.toxval_fix	If TRUE (default) read the dictionaries into the toxval_fix table

Value

The database will be altered

```
fix.associated.pod.critical_effect
```

Appends associated POD information to critical_effect for derived toxval_types

Description

Appends associated POD information to critical_effect for derived toxval_types

Usage

```
fix.associated.pod.critical_effect(res, map_fields)
```

Arguments

res	The data to be altered
map_fields	The fields used to map entries to associated PODs

fix.casrn

fix.casrn

Description

Fix a CASRN that has one of several problems

Usage

```
fix.casrn(casrn, cname = "", verbose = FALSE)
```

Arguments

casrn	Input CASRN to be fixed
cname	An optional chemical name
verbose	if TRUE, print the input values

Details

DETAILS

Value

the fixed CASRN

See Also

[reexports](#)

Examples

```
## Not run:
if(interactive()){
  fix.casrn("107028")
  # Expected output "107-02-8"
}

## End(Not run)
```

```
fix.critical_effect.icf.by.source
```

*standardize critical_effect in toxval table based on icf dictionary and
toxval critical effects dictionary*

Description

standardize critical_effect in toxval table based on icf dictionary and toxval critical effects dictionary

Usage

```
fix.critical_effect.icf.by.source(toxval.db, source, subsource = NULL)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	The source to be fixed
subsource	The subsource to be fixed (NULL default)

```
fix.dedup.hierarchy.by.source
```

Set qc_status as "fail" for lesser priority duplicates

Description

Set qc_status as "fail" for lesser priority duplicates

Usage

```
fix.dedup.hierarchy.by.source(
  toxval.db,
  source = NULL,
  subsource = NULL,
  priority_list = NULL,
  subsource_priority_list = NULL,
  criteria = c("dtxsid"),
  report.only = FALSE
)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	Source to be fixed
subsource	Subsource to be fixed (NULL default)
priority_list	Named list describing source priority, with low priority index and high priority value
subsource_priority_list	Named list of subsources to deprecate per source, source index/subsource value
criteria	List of parameters used to make deduping decisions
report.only	Whether to report or write/export data. Default is FALSE (write/export data)

fix.derived.toxval_type.by.source

Set select normalized toxval fields to '-' if the record is a select toxval_type

Description

Set select normalized toxval fields to '-' if the record is a select toxval_type

Usage

```
fix.derived.toxval_type.by.source(
  toxval.db,
  source = NULL,
  subsource = NULL,
  report.only = FALSE
)
```

Arguments

toxval.db	The version of the database to use
source	The source to be fixed
subsource	The subsource to be fixed (NULL default)
report.only	Whether to update database or only report the results. Default FALSE.

fix.empty.by.source	Set all empty cells in toxval to '-'
---------------------	--------------------------------------

Description

Set all empty cells in toxval to '-'

Usage

```
fix.empty.by.source(toxval.db, source = NULL, subsources = NULL)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed
subsources	The subsources to be fixed (NULL default)

Value

The database will be altered

fix.empty.record_source.by.source	Set all empty cells in record_source to '-'
-----------------------------------	---

Description

Set all empty cells in record_source to '-'

Usage

```
fix.empty.record_source.by.source(toxval.db, source = NULL)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed

Value

The database will be altered

fix.exposure.params	<i>Fix the exposure fields: exposure_method, exposure_route, exposure_form based on a 3 column dictionary ~/dictionary/exposure_route_method_form.xlsx</i>
---------------------	--

Description

Fix the exposure fields: exposure_method, exposure_route, exposure_form based on a 3 column dictionary ~/dictionary/exposure_route_method_form.xlsx

Usage

```
fix.exposure.params(
  toxval.db,
  source = NULL,
  subsource = NULL,
  report.only = FALSE
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If source=NULL, fix all sources
subsource	The subsource to be fixed (NULL default)
report.only	Whether to report or write/export data. Default is FALSE (write/export data)
fill.toxval_fix	If TRUE (default) read the dictionaries into the toxval_fix table

Value

The database will be altered (if report.only=TRUE, return missing entries)

fix.generation.by.source	<i>Alter the contents of toxval according to an excel dictionary file with field generation</i>
--------------------------	---

Description

Alter the contents of toxval according to an excel dictionary file with field generation

Usage

```
fix.generation.by.source(toxval.db, source, subsource = NULL)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be processed
subsource	The subsource to be processed (NULL default)

Value

The database will be altered

```
fix.human_eco.by.source
```

Fix the human_eco flag

Description

Fix the human_eco flag

Usage

```
fix.human_eco.by.source(toxval.db, source = NULL, subsource = NULL)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If NULL, fix all sources
subsource	The subsource to be fixed (NULL default)

Value

The database will be altered

```
fix.non_ascii.v2
```

fix.non_ascii.v2

Description

Flag and fix non-ascii characters in the database

Usage

```
fix.non_ascii.v2(df, source)
```


Arguments

df	The dataframe to be processed
source	Current ToxVal source
The	source to be fixed

Details

DETAILS

Value

The dataframe with non ascii characters replaced with cleaned versions

See Also

[read.xlsx](#), [write.xlsx](#) [str_trim](#) [stri_escape_unicode](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

fix.priority_id.by.source
<i>Fix the priority_id in the toxval table based on source</i>

Description

Fix the priority_id in the toxval table based on source

Usage

```
fix.priority_id.by.source(toxval.db, source = NULL, subsources = NULL)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	The source to be fixed, If NULL, set for all sources
subsources	The subsources to be fixed (NULL default)

```
fix.qc_status.by.source
```

Fix the qa_status flag

Description

Fix the qa_status flag

Usage

```
fix.qc_status.by.source(
  toxval.db,
  source.db,
  source = NULL,
  subsources = NULL,
  reset = FALSE
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed
subsources	The subsources to be fixed (NULL default)
reset	If TRUE, reset all values to 'pass' before setting
sourcedb	The source database name

Value

The database will be altered

```
fix.replace.unicode    fix.replace.unicode
```

Description

A function to check all character fields and handle unicode symbols, either by removing them or replacing them with alphabetic equivalents.

Usage

```
fix.replace.unicode(df)
```

Arguments

df	Character vector to check/replace unicode symbols.
----	--

Details

DETAILS

Value

Returns a modified version of the input vector with unicode replacements.

See Also

[stri_escape_unicode][stringi::stri_escape_unicode] [str_extract][stringr::str_extract]

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

```
fix.risk_assessment_class.by.source
```

*Set the risk assessment class of toxval according to an excel dictionary.
Values may beset multiple times, so the excel sheet should be ordered
so that the last ones to be set are last*

Description

Set the risk assessment class of toxval according to an excel dictionary. Values may beset multiple times, so the excel sheet should be ordered so that the last ones to be set are last

Usage

```
fix.risk_assessment_class.by.source(
  toxval.db,
  source = NULL,
  subsource = NULL,
  restart = TRUE,
  report.only = FALSE
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be updated
subsource	The subsource to be updated (NULL default)
restart	If TRUE, delete all values and start from scratch
report.only	Whether to report or write/export data. Default is FALSE (write/export data)

```
fix.single.param.by.source
```

Alter the contents of toxval according to an excel dictionary

Description

Alter the contents of toxval according to an excel dictionary

Usage

```
fix.single.param.by.source(  
  toxval.db,  
  param,  
  source,  
  subsource = NULL,  
  ignore = FALSE,  
  report.only = FALSE,  
  units.data = NULL  
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
param	The parameter value to be fixed
source	The source to be fixed
subsource	The subsource to be fixed (NULL default)
ignore	If TRUE allow missing values to be ignored
report.only	Whether to report or write/export data. Default is FALSE (write/export data)
units.data	A dataframe containing current units data if units are to be reported (NULL default)

Value

The database will be altered

```
fix.species.common_name
```

Fix issues with species common names

Description

Fix issues with species common names

Usage

```
fix.species.common_name(toxval.db)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
-----------	---

```
fix.species.duplicates
```

Check for species duplicates - same common name but multiple species_ids

Description

Check for species duplicates - same common name but multiple species_ids

Usage

```
fix.species.duplicates(toxval.db, source = NULL, subsource = NULL)
```

Arguments

toxval.db	The version of the database to use
source	The source to be checked. If source=NULL, check all sources
subsource	The subsource to be checked (NULL default)

```
fix.species.v2
```

Set the species_id column in toxval

Description

This function replaces fix.species This function precedes toxvaldb.load.species

Usage

```
fix.species.v2(  
  toxval.db,  
  source = NULL,  
  subsource = NULL,  
  date_string = "2023-05-18"  
)
```

Arguments

toxval.db	The version of the database to use
source	The source to be fixed
subsource	The subsource to be fixed (NULL default)
date_string	The date version of the dictionary

fix.strain.v2	<i>Set the strain information in toxval</i>
---------------	---

Description

Set the strain information in toxval

Usage

```
fix.strain.v2(  
  toxval.db,  
  source = NULL,  
  subsource = NULL,  
  date_string = "2024-04-08",  
  reset = FALSE  
)
```

Arguments

toxval.db	The version of the database to use
source	The source to be fixed. If NULL, fix for all sources
subsource	The subsource to be fixed (NULL default)
date_string	The date of the latest dictionary version

fix.study_duration.params	<i>Fix the study duration fields: study_duration_value, study_duration_units, study_duration_class based on a 3 column dictionary ~/dictionary/exposure_route_method_form.xlsx</i>
---------------------------	--

Description

Fix the study duration fields: study_duration_value, study_duration_units, study_duration_class based on a 3 column dictionary ~/dictionary/exposure_route_method_form.xlsx

Usage

```
fix.study_duration.params(
  toxval.db,
  source = NULL,
  subsources = NULL,
  report.only = FALSE
)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If source=NULL, fix all sources
subsources	The subsources to be fixed (NULL default)
report.only	Whether to report or write/export data. Default is FALSE (write/export data)
fill.toxval_fix	If TRUE (default) read the dictionaries into the toxval_fix table

Value

The database will be altered

fix.study_group	<i>Set the study_group field</i>
-----------------	----------------------------------

Description

Set the study_group field

Usage

```
fix.study_group(
  toxval.db,
  source = NULL,
  subsources = NULL,
  report.only = FALSE
)
```

Arguments

toxval.db	Database version
source	The source to be updated
subsources	The subsources to be updated (NULL default)
report.only	Whether to apply study_group fix or just report what fixes would be applied.

Value

for each source writes an Excel file with the name ../export/export_by_source_data/toxval_all_toxval.db_source.xlsx

fix.study_type.by.source

Fix the study_type using manual curation on a source-by-source basis

Description

This function replaces the original `export.for_study_type` and `fix.study_type.manual`, with the intention of making it easier to fix the study types on a source-by-source basis. All of the work will happen in the directory `~/Repo/dictionary/study_type_by_source`. Each source will have its own file and will not have a date attached to make maintenance easier. To start the process, run this with `mode="export"`. This will write a source-specific file to the `export_temp` directory. Open either the `xlsx` or `csv` (if the `xlsx` is corrupted) and place this file into the main directory (`study_type_by_source`) and edit it there as documented in the main documentation. Next run this function with `mode="import"`. This will load your changes into the database. It is suggested that before working on a new source that the old version in the `study_type_by_source` get pushed to the `old_versions` directory.

Usage

```
fix.study_type.by.source(
    toxval.db,
    mode = "export",
    source = NULL,
    subsources = NULL,
    custom.query.filter = NULL,
    report.only = FALSE
)
```

Arguments

<code>toxval.db</code>	The version of <code>toxval</code> in which the data is altered.
<code>mode</code>	Either <code>export</code> or <code>import</code>
<code>source</code>	The source you want to work on. If <code>NULL</code> , this will run all sources
<code>subsources</code>	The subsources to be fixed
<code>custom.query.filter</code>	Additional filters for the query. Example: <code>custom.query.filter = paste0(" and b.human_eco='human health' and ", "e.toxval_type_supercategory in ('Point of Departure','Lethality Effect Level','Toxicity Value'))"</code>
<code>report.only</code>	Whether to report or write/export data. Default is <code>FALSE</code> (write/export data)

Value

The database will be altered

fix.trim_spaces	<i>Trim leading and trailing blanks from all character columns</i>
-----------------	--

Description

Trim leading and trailing blanks from all character columns

Usage

```
fix.trim_spaces(res)
```

Arguments

toxval.db	The version of toxval in which the data is altered.
source	The source to be fixed. If source=NULL, fix all sources
fill.toxval_fix	If TRUE (default) read the dictionaries into the toxval_fix table

Value

The database will be altered

fix.units.by.source	<i>Do all of the fixes to units</i>
---------------------	-------------------------------------

Description

1. All of these steps operate on the toxval_units column.
2. Replace variant unit names with standard ones, running fix.single.param.new.by.source.R This fixes issues like variant names for mg/kg-day and uses the dictionary file dictionary/toxval_units_5.xlsx
3. Fix special characters in toxval_units
4. Fix issues with units containing extra characters for some ECOTOX records
5. Convert units that are multiples of standard ones (e.g. ppb to ppm). This uses the dictionary file dictionary/toxval_units conversions 2018-09-12.xlsx
6. Run conversions from molar to mg units, using MW. This uses the dictionary file dictionary/MW conversions.xlsx
7. Convert ppm to mg/m3 for inhalation studies. This uses the conversion Concentration (mg/m3) = 0.0409 x concentration (ppm) x molecular weight. See <https://cfpub.epa.gov/ncer/abstracts/index.cfm/fuseaction/dispatch> This function requires that the DSSTox external chemical_id be set
8. Convert ppm to mg/kg-day in toxval according to a species-specific conversion factor for oral exposures. This uses the dictionary file dictionary/ppm to mgkgday by animal.xlsx See: www10.plala.or.jp/biostatistics/1-3.doc This probably assumes feed rather than water
9. Make sure that eco studies are in mg/L and human health in mg/m3

Usage

```
fix.units.by.source(
  toxval.db,
  source = NULL,
  subsource = NULL,
  do.convert.units = FALSE,
  report.only = FALSE,
  report.extra = FALSE
)
```

Arguments

<code>toxval.db</code>	The version of toxvaldb to use.
<code>source</code>	Source to be fixed
<code>subsource</code>	Subsource to be fixed (NULL default)
<code>do.convert.units</code>	If TRUE, so unit conversions, as opposed to just cleaning
<code>report.only</code>	Whether to report or write/export data. Default is FALSE (write/export data)
<code>report.extra</code>	If reporting, then choose whether to record extra conversion information (e.g. <code>toxval_type</code> , <code>mw</code> , <code>species_id</code> , etc.)

<code>generate.originals</code>	<i>Duplicate any columns with '_original' Set Toxval Defaults</i>
---------------------------------	---

Description

Duplicate any columns with '_original' Set Toxval Defaults

Usage

```
generate.originals(toxval.db, mat)
```

Arguments

<code>toxval.db</code>	The version of toxval from which to set defaults.
<code>mat</code>	The matrix of data to be altered

Value

The altered input matrix

`getDBConn`*getDBConn*

Description

Get the names the database server, user, and pass or returns error message

Usage

```
getDBConn()
```

Details

DETAILS

Value

print the database connection information

Examples

```
## Not run:  
if(interactive()){  
  #EXAMPLE1  
}  
  
## End(Not run)
```

`import.dictionary`*import the toxval and toxval_type dictionaries*

Description

import the toxval and toxval_type dictionaries

Usage

```
import.dictionary(toxval.db)
```

Arguments

`toxval.db` The name of the database

<code>import.source.info.by.source</code>	<i>Load Source Info for each source into toxval The information is in the file ~/dictionary/source_info 2023-11-30.xlsx</i>
---	---

Description

Load Source Info for each source into toxval The information is in the file ~/dictionary/source_info 2023-11-30.xlsx

Usage

```
import.source.info.by.source(  
    toxval.db,  
    source = NULL,  
    dict_date = "2024-08-28"  
)
```

Arguments

<code>toxval.db</code>	The version of toxval into which the source info is loaded.
<code>source</code>	The specific source to be loaded, If NULL, load for all sources
<code>dict_date</code>	Date stamp of the dictionary file to update

<code>load.dsstox</code>	<i>Load DSSTox if needed from a file into a global variables (DSSTOX)</i>
--------------------------	---

Description

Load DSSTox if needed from a file into a global variables (DSSTOX)

Usage

```
load.dsstox(reprocess = FALSE)
```

log_message	<i>Function to combine output log with output message</i>
-------------	---

Description

Function to combine output log with output message

Function to combine output log with output message

Usage

```
log_message(log_df, message_df_col)
```

```
log_message(log_df, message_df_col)
```

Arguments

log_df Dataframe to which the log information will be appended

message_df_col New message to add

printCurrentFunction	<i>printCurrentFunction</i>
----------------------	-----------------------------

Description

Print the name of the current function

Usage

```
printCurrentFunction(comment.string = NA)
```

Arguments

comment.string An optional string to be printed

Details

DETAILS

Value

None

See Also

[flush.console](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

pull_jira_info	<i>pull_jira_info</i>
----------------	-----------------------

Description

Script to process CSV export of Jira into a status log

Usage

```
pull_jira_info(
  jira_project = "TOXVAL",
  in_file = NULL,
  auth_token = NULL,
  ticket_filter_list = NULL
)
```

Arguments

- jira_project Jira project code (e.g. CVTDB)
- in_file File path to Jira ticket summary CSV.
- auth_token Authorization token for Jira
- ticket_filter_list
 List of Jira tickets to filter to

Details

DETAILS

Value

Summary DataFrame of Jira tickets by Epic, Label, and Status

See Also

```
[download.file][utils::download.file], [unzip][utils::unzip] [read_csv][readr::read_csv], [cols][readr::cols]
[select][dplyr::select], [contains][dplyr::contains], [mutate][dplyr::mutate], [everything][dplyr::everything],
[filter][dplyr::filter], [distinct][dplyr::distinct], [left_join][dplyr::left_join], [group_by][dplyr::group_by],
[summarise][dplyr::summarise], [n][dplyr::n] [unite][tidyr::unite] [str_squish][stringr::str_squish]
```

Examples

```
## Not run:
if(interactive()){
  out = pull_jira_info(jira_project="project_name")
}

## End(Not run)
```

qa_toxval_url_validation
<i>qa_toxval_url_validation</i>

Description

Function to pull URLs and log their HTTP statuses

Usage

```
qa_toxval_url_validation(
  tbl_list = c("toxval", "record_source", "source_info"),
  db,
  log_suffix
)
```

Arguments

tbl_list	List of ToxVal tables to pull URLs from, Default: c("toxval", "record_source", "source_info")
db	ToxVal database name to pull URLs from
log_suffix	Suffix to add to end of log file to uniquely identify file, Default: Date stamp from Sys.Date()

Details

DETAILS

Value

None. Log file is generated

See Also

[read_excel](#), [filter](#), [mutate](#), [reexports](#), [bind_pivot_longer](#) [keep](#) [GET](#), [status_code](#) [write_xlsx](#)

Examples

```
## Not run:
if(interactive()){
  qa_toxval_url_validation(tbl_list = c("toxval", "record_source", "source_info"), db="res_toxval_v94", log_suffix="")
}

## End(Not run)
```

runInsert	<i>runInsert</i>
-----------	------------------

Description

Insert a record into a database. if auto.increment=TRUE, return the auto incremented primary key of the record. otherwise, return -1

Usage

```
runInsert(query, db, do.halt = F, verbose = F, auto.increment.id = F)
```

Arguments

- query a properly formatted SQL query as a string
- db the name of the database
- do.halt if TRUE, halt on errors or warnings
- verbose if TRUE, print diagnostic information
- auto.increment.id PARAM_DESCRIPTION, Default: F
- auto.increment if TRUE, add the auto increment primary key even if not part of the query

Details

DETAILS

Value

Returns the database table auto incremented primary key ID

See Also

```
character\(0\), MySQLDriver-class
```


Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

runInsertTable

runInsertTable

Description

Inserts multiple rows into a database table

Usage

```
runInsertTable(mat, table, db, do.halt = TRUE, verbose = FALSE, get.id = TRUE)
```

Arguments

mat	data frame containing the data, with the column names corresponding
table	name of the database table to which data will be inserted
db	the name of the database
do.halt	if TRUE, halt on errors or warnings
verbose	if TRUE, print diagnostic information
get.id	Whether to return ID or not, Default: T

Details

DETAILS

Value

ID or None

See Also

[character\(0\)](#), [MySQLDriver-class](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

runQuery

runQuery

Description

Runs a database query and returns a result set

Usage

```
runQuery(query = NULL, db, do.halt = TRUE, verbose = FALSE)
```

Arguments

query	a properly formatted SQL query as a string
db	the name of the database
do.halt	if TRUE, halt on errors or warnings
verbose	if TRUE, print diagnostic information

Details

DETAILS

Value

Query results

See Also

[character\(0\), MySQLDriver-class flush.console](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

runStatement	<i>runStatement</i>
--------------	---------------------

Description

Run a SQL statement, such as an ALTER or UPDATE

Usage

```
runStatement(query, db, do.halt = FALSE, verbose = FALSE)
```

Arguments

query	a properly formatted SQL query as a string
db	the name of the database
do.halt	if TRUE, halt on errors or warnings
verbose	if TRUE, print diagnostic information

Details

DETAILS

Value

None. SQL statement is run.

See Also

[character\(0\)](#), [MySQLDriver-class](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

<code>runUpdate</code>	<i>runUpdate</i>
------------------------	------------------

Description

Runs a database query and returns a result set

Usage

```
runUpdate(  
    table,  
    updateQuery = NULL,  
    updated_df = NULL,  
    db,  
    do.halt = TRUE,  
    verbose = FALSE,  
    trigger_check = TRUE  
)
```

Arguments

<code>table</code>	table to update
<code>updateQuery</code>	a properly formatted SQL query as a string in the form of an UPDATE INNER JOIN
<code>updated_df</code>	a dataframe of updated data to temporarily write to database for INNER JOIN
<code>db</code>	the name of the database
<code>do.halt</code>	if TRUE, halt on errors or warnings
<code>verbose</code>	if TRUE, print diagnostic information
<code>trigger_check</code>	if FALSE, audit triggers are ignored/bypassed

Details

DETAILS

Value

None

See Also

[character\(0\), MySQLDriver-class dbSendStatement](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

```
set.critical_effect_category
```

Sets the final category for each term/study_type pair in the critical_effect_terms table

Description

Sets the final category for each term/study_type pair in the critical_effect_terms table

Usage

```
set.critical_effect_category(toxval.db)
```

Arguments

toxval.db The version of toxval into which the tables are loaded.

Value

None. SQL update statement is performed

```
set.experimental_record.by.source
```

Sets experimental_record flag by source for records in toxval

Description

Sets experimental_record flag by source for records in toxval

Usage

```
set.experimental_record.by.source(toxval.db, source = NULL)
```

Arguments

toxval.db The version of toxval into which the tables are loaded.

source Name of source to set. Default NULL means set experimental record for all sources

Value

None. SQL update statement is performed

set.initial.qc_status *Set toxval qc_status to source table qc_status*

Description

Set toxval qc_status to source table qc_status

Usage

```
set.initial.qc_status(toxval.db, source.db, source, subsource = NULL)
```

Arguments

toxval.db	The database version to use
source.db	The source database name
source	The source name
subsource	The subsource to update, if desired (Default: NULL)

set.qc.category.by.source
Function for assigning QC Categories to sources in toxval via the qc_category field

Description

Function for assigning QC Categories to sources in toxval via the qc_category field

Usage

```
set.qc.category.by.source(  
  toxval.db,  
  source.db,  
  source = NULL,  
  confluence_url = "https://confluence.epa.gov/x/VuCkFg",  
  confluence_access_token,  
  jira_access_token  
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
source	The source to set a qc_category for
confluence_url	URL to QC tracking Confluence page
confluence_access_token	A personal access token for authentication in Confluence
jira_access_token	A personal access token for authentication in Jira

```
set.study_type.by.study_group
```

Normalize study_type within study_group

Description

Normalize study_type within study_group

Usage

```
set.study_type.by.study_group(
  toxval.db,
  source = NULL,
  subsource = NULL,
  report.only = TRUE,
  filter.matching = FALSE
)
```

Arguments

toxval.db	The version of toxvaldb to use.
source	Source to check
subsource	Subsource to check (NULL default)
report.only	Whether to alter ToxVal (FALSE) or simply record suggestions (TRUE), default TRUE
filter.matching	Whether to ignore entries whose current study_type matches suggestion, default FALSE

set.supersource.export.names
<i>Populate export_source_name and supersource fields in ToxVal</i>

Description

Populate export_source_name and supersource fields in ToxVal

Usage

```
set.supersource.export.names(  
    toxval.db,  
    source = NULL,  
    version_date = "2024-08-28"  
)
```

Arguments

toxval.db	The version of toxval from which to set defaults.
source	The source to be fixed (if NULL then edit all sources)
version_date	The date of the source_info dictionary to be used

set_extraction_doc_clowder_id
<i>Inserts clowder document information into record_source table</i>

Description

Inserts clowder document information into record_source table

Usage

```
set_extraction_doc_clowder_id(toxval.db, source.db, source = NULL)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
source	Name of source to set. Default NULL means set Clowder ID for all sources

Value

None. SQL insert statement is performed

`set_toxval_relationship_by_toxval_type`*Generic function for setting record relationships based on standardized rules*

Description

Generic function for setting record relationships based on standardized rules

Usage

```
set_toxval_relationship_by_toxval_type(res, toxval.db)
```

Arguments

<code>res</code>	The data that has relationships to be represented
<code>toxval.db</code>	The version of toxval into which the tables are loaded.

`source_chemical.chemidplus`*special process to deal with source chemicals for ChemIDPlus*

Description

special process to deal with source chemicals for ChemIDPlus

Usage

```
source_chemical.chemidplus(  
  toxval.db,  
  source.db,  
  res,  
  source,  
  chem.check.halt = FALSE,  
  casrn.col = "casrn",  
  name.col = "name",  
  verbose = F  
)
```

Arguments

toxval.db	The version of toxval into which the source info is loaded.
source.db	The source database version
source	The xource to be processed (ECOTOX)
chem.check.halt	If TRUE, halt if there are errors in the chemical checking
casrn.col	Name of the column containing the CASRN
name.col	Name of the column containing chemical names
verbose	If TRUE, output extra diagnostics information

source_chemical.ecotox

special process to deal with source chemicals for ECOTOX

Description

special process to deal with source chemicals for ECOTOX

Usage

```
source_chemical.ecotox(
  toxval.db,
  source.db,
  res,
  source,
  chem.check.halt = FALSE,
  casrn.col = "casrn",
  name.col = "name",
  verbose = F
)
```

Arguments

toxval.db	The version of toxval into which the source info is loaded.
source.db	The source database version
source	The xource to be processed (ECOTOX)
chem.check.halt	If TRUE, halt if there are errors in the chemical checking
casrn.col	Name of the column containing the CASRN
name.col	Name of the column containing chemical names
verbose	If TRUE, output extra diagnostics information

source_chemical.extra	<i>special process to deal with source chemicals for extra source (cancer, genetox, skin_eye, etc)</i>
-----------------------	--

Description

special process to deal with source chemicals for extra source (cancer, genetox, skin_eye, etc)

Usage

```
source_chemical.extra(  
  toxval.db,  
  source.db,  
  res,  
  source,  
  chem.check.halt = FALSE,  
  casrn.col = "casrn",  
  name.col = "name",  
  verbose = FALSE  
)
```

Arguments

toxval.db	The version of toxval into which the source info is loaded.
source.db	The source database version
source	The source to be processed #' @param chem.check.halt If TRUE, halt if there are errors in the chemical checking
casrn.col	Name of the column containing the CASRN
name.col	Name of the column containing chemical names
verbose	If TRUE, output extra diagnostics information

source_chemical.toxrefdb	<i>Special process to deal with source chemicals for ToxRefDB. This will put the chemicals into the source database source_chemical table</i>
--------------------------	---

Description

Special process to deal with source chemicals for ToxRefDB. This will put the chemicals into the source database source_chemical table

Usage

```
source_chemical.toxrefdb(  
  toxval.db,  
  source.db,  
  res,  
  source = "ToxRefDB",  
  chem.check.halt = FALSE,  
  casrn.col = "casrn",  
  name.col = "name",  
  verbose = FALSE  
)
```

Arguments

toxval.db	The version of toxval into which the source info is loaded.
source.db	The source database version
res	The dataframe to which the chemical_id will be added
source	The name of the source
chem.check.halt	If TRUE, stop if there are problems with the chemical mapping
casrn.col	The name of the column containing the CASRN
name.col	The name of the column containing the chemical name
verbose	If TRUE, write out diagnostic messages

Value

Returns the input dataframe with the chemical_id added

source_hash_vectorized

source_hash_vectorized

Description

Generate the hash key for a source table based on hashing columns

Usage

```
source_hash_vectorized(res, hashing_cols)
```

Arguments

res	The data frame to be processed
hashing_cols	Optional list of columns to use for generating source_hash

Details

DETAILS

Value

Input dataframe with new source_hash field

See Also

[digest distinct](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

species.qc	<i>Run some checks on the species information</i>
------------	---

Description

Run some checks on the species information

Usage

species.qc(toxval.db)

Arguments

toxval.db The version of toxval into which the tables are loaded.

species.strain.mismatch	<i>Find species and strain mismaps</i>
-------------------------	--

Description

Find species and strain mismaps

Usage

species.strain.mismatch(toxval.db)

Arguments

toxval.db Database version

Value

Write a file with the results

toxval.config	<i>toxval.config</i>
---------------	----------------------

Description

Define a set of global variables. These include the source path (datapath) and the source databases (e.g. dev_toxval_version and dev_toxval_source_version).

Usage

toxval.config()

Details

DETAILS

Value

Returns a set of parameters to be used throughout the package

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

toxval.init.db	<i>Initialize the database. This will load the species, info and dictionary tables</i>
----------------	--

Description

Initialize the database. This will load the species, info and dictionary tables

Usage

```
toxval.init.db(toxval.db, version_info, reset = F, date_string = "2022-05-25")
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
version_info	Info string describing the version.
reset	If TRUE, delete all content from the database
date_string	The date of the dictionary versions

toxval.load.alaska_dec	<i>Load the alaska_dec (old ACToR - flex) data from toxval sourcedb to toxval</i>
------------------------	---

Description

Load the alaska_dec (old ACToR - flex) data from toxval sourcedb to toxval

Usage

```
toxval.load.alaska_dec(toxval.db, source.db, log = F)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, output log information to a file

<code>toxval.load.all</code>	<i>Load and process all information into ToxValDB. The entire process can be run with one command: <code>toxval.load.all(toxval.db=...,source.db=..., do.all=TRUE)</code> It can also be run in stages, but needs to be run in the order of the <code>do.X</code> parameters listed here. If any earlier step is run, all of the subsequent steps need to be rerun.</i>
------------------------------	---

Description

Load and process all information into ToxValDB. The entire process can be run with one command: `toxval.load.all(toxval.db=...,source.db=..., do.all=TRUE)` It can also be run in stages, but needs to be run in the order of the `do.X` parameters listed here. If any earlier step is run, all of the subsequent steps need to be rerun.

Usage

```
toxval.load.all(
  toxval.db,
  source.db,
  confluence_access_token,
  jira_access_token,
  log = FALSE,
  do.init = FALSE,
  do.reset = FALSE,
  do.load = FALSE,
  do.post = FALSE,
  do.extra = FALSE
)
```

Arguments

<code>toxval.db</code>	The version of toxval into which the tables are loaded.
<code>source.db</code>	The version of toxval_source database from which information is pulled.
<code>confluence_access_token</code>	A personal access token for authentication in Confluence
<code>jira_access_token</code>	A personal access token for authentication in Jira
<code>log</code>	If TRUE write the output from each load script to a log file
<code>do.init</code>	If True, clean out all of the database tables
<code>do.reset</code>	If TRUE, empty the database to restart
<code>do.load</code>	If TRUE, load all of the source
<code>do.post</code>	If TRUE, do th post-processingwork of fixing study type and risk_assessment_class
<code>do.extra</code>	If TRUE, load the non-toxval data (genetox, bcfbaf, skin/eye)

Value

Nothing is returned

```
toxval.load.atsdr.pfas.2021
```

Load data ATSDR PFAS 2021 data from toxval_source to toxval

Description

Load data ATSDR PFAS 2021 data from toxval_source to toxval

Usage

```
toxval.load.atsdr.pfas.2021(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.atsdr.mrls
```

Load the ATSDR MRLs data from toxval_source to toxval

Description

Load the ATSDR MRLs data from toxval_source to toxval

Usage

```
toxval.load.atsdr.mrls(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.caloeehha	<i>Load new_caloeehha from toxval_source to toxval</i>
-----------------------	--

Description

Load new_caloeehha from toxval_source to toxval

Usage

```
toxval.load.caloeehha(
  toxval.db,
  source.db,
  log = FALSE,
  remove_null_dtxsid = TRUE
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.cancer	<i>prepare the cancer call data. The data comes form a series of files ../NIOSH/NIOSH_CARC_2018.xlsx ../IRIS/iris_cancer_call_2018-10-03.xlsx ../PPRTV_ORNL/PPRTV_ORNL cancer calls 2018-10-25.xlsx ../cancer_summary/cancer/NTP/NTP cancer clean.xlsx ../cancer_summary/cancer/IARC/IARC cancer 2018-10-29.xlsx ../cancer_summary/cancer/HealthCanada/HealthCanada_TRVs_2010_AppendixA v2.xlsx ../cancer_summary/cancer/EPA_OPP_CARC/EPA_CARC.xlsx ../cancer_summary/cancer/CalEPA/calepa_p65_cancer_only.xlsx</i>
--------------------	--

Description

extract all of the chemicals with cancer slope factor or unit risk with appropriate units

Usage

```
toxval.load.cancer(toxval.db, source.db)
```

Arguments

toxval.db	The version of the database to use
-----------	------------------------------------

```
toxval.load.chemidplus
```

Load ChemID Plus Acute data to toxval

Description

Load ChemID Plus Acute data to toxval

Usage

```
toxval.load.chemidplus(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE,  
  do.init = FALSE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value
do.init	if TRUE, read the data in from the file and set up the matrix

toxval.load.copper	<i>Load Copper Manufacturers data to toxval from toxval_source</i>
--------------------	--

Description

Load Copper Manufacturers data to toxval from toxval_source

Usage

```
toxval.load.copper(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

- | | |
|--------------------|---|
| toxval.db | The database version to use |
| source.db | The source database |
| log | If TRUE, send output to a log file |
| remove_null_dtxsid | If TRUE, delete source records without curated DTXSID value |

toxval.load.dedup	<i>toxval.load.dedup</i>
-------------------	--------------------------

Description

Perform deduping on data before it is loaded to toxval

Usage

```
toxval.load.dedup(  
  res,  
  dedup_fields = NULL,  
  hashing_cols = toxval.config()$hashing_cols,  
  delim = " |::| "  
)
```

Arguments

- | | |
|--------------|--|
| res | dataframe containing the source data to dedup |
| dedup_fields | vector containing field names to dedup, Default: NULL (all fields but hashing cols) |
| hashing_cols | vector containing field names of hashing columns, Default: toxval.config()\$hashing_cols |
| delim | string used to separate collapsed values, Default: ' :: ' |

Details

DETAILS

Value

dataframe containing deduped source data

See Also

[select](#), [group_by](#), [summarise](#), [context](#), [filter](#), [mutate](#), [across](#), [reexports](#), [na_if](#), [distinct](#)

Examples

```
## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)
```

toxval.load.dod	<i>Load the DOD data from toxval_source to toxval</i>
-----------------	---

Description

Load the DOD data from toxval_source to toxval

Usage

```
toxval.load.dod(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

- toxval.db The version of toxval into which the tables are loaded.
- source.db The source database to use.
- log If TRUE, send output to a log file

`toxval.load.doe.benchmarks`*Load DOE Wildlife Benchmarks data from toxval_source to toxval*

Description

Load DOE Wildlife Benchmarks data from toxval_source to toxval

Usage

```
toxval.load.doe.benchmarks(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

<code>toxval.db</code>	The database version to use
<code>source.db</code>	The source database
<code>log</code>	If TRUE, send output to a log file
<code>remove_null_dtxsid</code>	If TRUE, delete source records without curated DTXSID value

`toxval.load.doe.pac`*Load DOE Protective Action Criteria data from toxval_source to toxval*

Description

Load DOE Protective Action Criteria data from toxval_source to toxval

Usage

```
toxval.load.doe.pac(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

`toxval.load.echa_iuclid`

Loading the ECHA IUCLID data to toxval from toxval_source This method is different from most because there are multiple tables (one per study type) for this source

Description

Loading the ECHA IUCLID data to toxval from toxval_source This method is different from most because there are multiple tables (one per study type) for this source

Usage

```
toxval.load.echa_iuclid(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.ecotox	<i>Load ECOTOX from the datahub to toxval</i>
--------------------	---

Description

Load ECOTOX from the datahub to toxval

Usage

```
toxval.load.ecotox(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE,  
  sys.date = "2024-05-30"  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value
sys.date	The version of the data to be used

toxval.load.efsa	<i>Load EFSA data from toxval_source to toxval</i>
------------------	--

Description

Load EFSA data from toxval_source to toxval

Usage

```
toxval.load.efsa(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file

toxval.load.epa_aegl *Load the EPA AEGL data from toxval_source to toxval*

Description

Load the EPA AEGL data from toxval_source to toxval

Usage

```
toxval.load.epa_aegl(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.epa_hhtv *Load EPA HHTV data to toxval from toxval_source*

Description

Load EPA HHTV data to toxval from toxval_source

Usage

```
toxval.load.epa_hhtv(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.epa_ow_npdwr

Loading EPA OW NPDWR to toxval from toxval_source

Description

Loading EPA OW NPDWR to toxval from toxval_source

Usage

```
toxval.load.epa_ow_npdwr(
  toxval.db,
  source.db,
  log = FALSE,
  remove_null_dtxsid = TRUE
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.epa_ow_nrwqc_hhc

Loading EPA OW NRWQC-HHC to toxval from toxval_source

Description

Loading EPA OW NRWQC-HHC to toxval from toxval_source

Usage

```
toxval.load.epa_ow_nrwqc_hhc(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.generic	<i>Generic structure for loading to toxval from toxval_source</i>
---------------------	---

Description

Generic structure for loading to toxval from toxval_source

Usage

```
toxval.load.generic(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.genetox.all
```

Load the Genetox data from Grace

Description

Load the Genetox data from Grace

Usage

```
toxval.load.genetox.all(  
  toxval.db,  
  source.db,  
  sys.date = "2021-09-10",  
  verbose = FALSE  
)
```

Arguments

toxval.db	The database to use.
source.db	The source database to use.
sys.date	The input file version
verbose	If TRUE output debug information

```
toxval.load.gestis.dnel
```

Load GESTIS DNEL data from toxval_source to toxval

Description

Load GESTIS DNEL data from toxval_source to toxval

Usage

```
toxval.load.gestis.dnel(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.hawc	<i>Load HAWC from toxval_source to toxval</i>
------------------	---

Description

Load HAWC from toxval_source to toxval

Usage

```
toxval.load.hawc(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.hawc_pfas_150	<i>Load HAWC PFAS 150 from toxval_source to toxval</i>
---------------------------	--

Description

Load HAWC PFAS 150 from toxval_source to toxval

Usage

```
toxval.load.hawc_pfas_150(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The version of toxval_source from which the tables are loaded.
log	If TRUE, send output to a log file
remove_null_dtgsid	If TRUE, delete source records without curated DTGSID value

```
toxval.load.hawc_pfas_430
```

Load HAWC PFAS 430 from toxval_source to toxval

Description

Load HAWC PFAS 430 from toxval_source to toxval

Usage

```
toxval.load.hawc_pfas_430(
  toxval.db,
  source.db,
  log = FALSE,
  remove_null_dtgsid = TRUE
)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The version of toxval_source from which the tables are loaded.
log	If TRUE, send output to a log file
remove_null_dtgsid	If TRUE, delete source records without curated DTGSID value

```
toxval.load.healthcanada
```

Load Health Canada data from toxval_source to toxval

Description

Generic structure for loading to toxval from toxval_source

Usage

```
toxval.load.healthcanada(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.heast	<i>Load the HEAST data from toxval_source to toxval</i>
-------------------	---

Description

Load the HEAST data from toxval_source to toxval

Usage

```
toxval.load.heast(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.hess	<i>Load HESS data to ToxVal</i>
------------------	---------------------------------

Description

Load HESS data to ToxVal

Usage

```
toxval.load.hess(toxval.db, source.db, log = FALSE, remove_null_dtgsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtgsid	If TRUE, delete source records without curated DTGSID value

toxval.load.hpvis	<i>Load HPVIS from toxval_source to toxval</i>
-------------------	--

Description

Load HPVIS from toxval_source to toxval

Usage

```
toxval.load.hpvis(toxval.db, source.db, log = FALSE, remove_null_dtgsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtgsid	If TRUE, delete source records without curated DTGSID value

toxval.load.initial	<i>Delete the contents of the toxval database</i>
---------------------	---

Description

Delete the contents of the toxval database

Usage

```
toxval.load.initial(toxval.db)
```

Arguments

toxval.db	The version of toxval from which the data is deleted.
-----------	---

toxval.load.iris	<i>Load IRIS source from toxval_source to toxval</i>
------------------	--

Description

Load IRIS source from toxval_source to toxval

Usage

```
toxval.load.iris(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.mass_mmcl	<i>Load the Mass. Drinking Water Standards data from toxval_source to toxval</i>
-----------------------	--

Description

Load the Mass. Drinking Water Standards data from toxval_source to toxval

Usage

```
toxval.load.mass_mmcl(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.niosh	<i>Load NIOSH from toxval_source to toxval</i>
-------------------	--

Description

Load NIOSH from toxval_source to toxval

Usage

```
toxval.load.niosh(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.ntp.pfas	<i>Load NTP PFAS data from toxval_source to toxval Generic structure for loading to toxval from toxval_source</i>
----------------------	---

Description

Load NTP PFAS data from toxval_source to toxval Generic structure for loading to toxval from toxval_source

Usage

```
toxval.load.ntp.pfas(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.opp	<i>Load EPA OPP data to toxval from toxval_source</i>
-----------------	---

Description

Load EPA OPP data to toxval from toxval_source

Usage

```
toxval.load.opp(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.osha_air_limits
```

Load the osha_air_limits (old ACToR - flex) data from toxval sourcedb to toxval

Description

Load the osha_air_limits (old ACToR - flex) data from toxval sourcedb to toxval

Usage

```
toxval.load.osha_air_limits(toxval.db, source.db, log = F)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file

```
toxval.load.ow_dwsha
```

Load the ow_dwsha data from toxval_source to toxval

Description

Load the ow_dwsha data from toxval_source to toxval

Usage

```
toxval.load.ow_dwsha(
  toxval.db,
  source.db,
  log = FALSE,
  remove_null_dtxsid = TRUE
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.penn	<i>Load Penn data from toxval_source to toxval</i>
------------------	--

Description

Load Penn data from toxval_source to toxval

Usage

```
toxval.load.penn(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
source.db	The source database to use.
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.penn_dep_mscs	<i>Load the penn_dep_mscs data from toxval_source to toxval</i>
---------------------------	---

Description

Load the penn_dep_mscs data from toxval_source to toxval

Usage

```
toxval.load.penn_dep_mscs(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.pfas_150_sem_v2
```

Load pfas_150_sem from toxval_source to toxval

Description

Load pfas_150_sem from toxval_source to toxval

Usage

```
toxval.load.pfas_150_sem_v2(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.postprocess
```

Do all of the post-processing steps for a source

Description

Do all of the post-processing steps for a source

Usage

```
toxval.load.postprocess(  
  toxval.db,  
  source.db,  
  source,  
  do.convert.units = FALSE,  
  chem_source,  
  subsource = NULL,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database name
source	The source name
do.convert.units	If TRUE, convert units, mainly from ppm to mg/kg-day. This code is not debugged
chem_source	Used only for source=ECHA IUCLID
subsource	The specific subsource to process, if desired (Default: NULL)
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

`toxval.load.pprtv.cphea`*Load PPRTV CPHEA from toxval_source to toxval*

Description

Load PPRTV CPHEA from toxval_source to toxval

Usage

```
toxval.load.pprtv.cphea(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.rsl	<i>Load the RSL data from source db to toxval - the source database needs to be updated periodically</i>
-----------------	--

Description

Load the RSL data from source db to toxval - the source database needs to be updated periodically

Usage

```
toxval.load.rsl(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.skin.ey	<i>Load the Skin eye data</i>
---------------------	-------------------------------

Description

Load the Skin eye data

Usage

```
toxval.load.skin.ey(toxval.db, source.db, verbose = FALSE)
```

Arguments

toxval.db	Database version
verbose	if TRUE, print diagnostic messages along the way

```
toxval.load.source_chemical
```

Perform the DSSTox mapping

Description

Perform the DSSTox mapping

Usage

```
toxval.load.source_chemical(  
    toxval.db,  
    source.db,  
    source = NULL,  
    verbose = TRUE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The version of toxvaldb to use.
source.db	The source database version
source	The source to update for
verbose	If TRUE, print out extra diagnostic messages
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

```
toxval.load.species
```

Load the species table

Description

Load the species table

Usage

```
toxval.load.species(toxval.db, date_string = "2023-05-18")
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
date_string	The date string for the dictionary files

toxval.load.test	<i>Load TEST data from toxval_source to toxval</i>
------------------	--

Description

Load TEST data from toxval_source to toxval

Usage

```
toxval.load.test(toxval.db, source.db, log = FALSE, remove_null_dtxsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.toxrefdb2.1	<i>Load ToxRefdb data to toxval</i>
-------------------------	-------------------------------------

Description

Load ToxRefdb data to toxval

Usage

```
toxval.load.toxrefdb2.1(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.usgs_hbsl	<i>Load the usgs_hbsl (old ACToR - flex) data from toxval source db to toxval</i>
-----------------------	---

Description

Load the usgs_hbsl (old ACToR - flex) data from toxval source db to toxval

Usage

```
toxval.load.usgs_hbsl(toxval.db, source.db, log = F)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file

toxval.load.ut_hb	<i>Load the uterotrophic and Hershberger data</i>
-------------------	---

Description

Load the uterotrophic and Hershberger data

Usage

```
toxval.load.ut_hb(toxval.db, source.db, log = FALSE, remove_null_dtgsid = TRUE)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtgsid	If TRUE, delete source records without curated DTGSID value

toxval.load.who_ipcs *Load the who_ipcs data from toxval source db to toxval*

Description

Load the who_ipcs data from toxval source db to toxval

Usage

```
toxval.load.who_ipcs(  
    toxval.db,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

toxval.load.who_jecfa_adi
 Load WHO JECFA ADI from toxval_source to toxval

Description

Load WHO JECFA ADI from toxval_source to toxval

Usage

```
toxval.load.who_jecfa_adi(  
    toxvaldb,  
    source.db,  
    log = FALSE,  
    remove_null_dtxsid = TRUE  
)
```

Arguments

source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value
toxval.db	The database version to use

`toxval.load.who_jecfa_tox_studies`*Load WHO JECFA Tox Studies from toxval_source to toxval*

Description

Load WHO JECFA Tox Studies from toxval_source to toxval

Usage

```
toxval.load.who_jecfa_tox_studies(  
  toxval.db,  
  source.db,  
  log = FALSE,  
  remove_null_dtxsid = TRUE  
)
```

Arguments

toxval.db	The database version to use
source.db	The source database
log	If TRUE, send output to a log file
remove_null_dtxsid	If TRUE, delete source records without curated DTXSID value

`toxval.set.mw`*Set the molecular weight in the toxval table, for use in unit conversions*

Description

Set the molecular weight in the toxval table, for use in unit conversions

Usage

```
toxval.set.mw(toxval.db, source = NULL, subsource = NULL)
```

Arguments

toxval.db	The database version to use
source	The source
subsource	The subsource

toxval.summary.stats	<i>Generate summary statistics on the toxval database</i>
----------------------	---

Description

Generate summary statistics on the toxval database

Usage

```
toxval.summary.stats(toxval.db)
```

Arguments

toxval.db	The version of toxval into which the tables are loaded.
-----------	---

toxvaldb.view	<i>Produce a view of the ToxValDB Data</i>
---------------	--

Description

‘toxvaldb.view’ Produces a view for ToxValDB by merging specified tables

Usage

```
toxvaldb.view(toxval.db, user, password, count = 10)
```

Arguments

toxval.db	Database version
user	The username for the MySQL database. The database instance is hard-coded in the function setDBConn().
password	The user’s MySQL database password.
count	If count>0, only select this number of records from each source, used for debugging

Value

Write a file with the results: data/view/ToxValDB View toxval.db Sys.Date().xlsx

toxval_type.species.mismatch
<i>Find species and toxval_type mismatches, e.g. species other than human from RfD, RfC, cancer sloper, MSL, etc.</i>

Description

Find species and toxval_type mismatches, e.g. species other than human from RfD, RfC, cancer sloper, MSL, etc.

Usage

toxval_type.species.mismatch(toxval.db)

Arguments

toxval.db	Database version
source	The source to be updated

Value

Write a file with the results

%>%	<i>Pipe operator</i>
-----	----------------------

Description

See `magrittr::%>%` for details.

Usage

lhs %>% rhs

Arguments

lhs	A value or the magrittr placeholder.
rhs	A function call using the magrittr semantics.

Value

The result of calling 'rhs(lhs)'.

Index

- * **cas_functions**
 - cas_checkSum, 5
- * **internal**
 - %>%, 87
- %>%, 87, 87
- across, 61
- bind, 39
- cas_checkSum, 5
- cas_detect, 5
- character(0), 40–44
- check.toxval_type.route.units, 6
- chem.check.v2, 7
- clean.last.character, 7
- clean.toxval.by.source, 8
- compare.versions, 9
- context, 61
- dbSendStatement, 44
- digest, 53
- distinct, 53, 61
- duplicate.hunter, 9
- ecotox.select.study.duration, 10
- ecotox.select.toxval.numeric, 10
- ecotox.species.dictionary, 11
- export.all.by.source, 11
- export.for.missing.species, 12
- export.for.oppt, 12
- export.for.toxval.qc, 13
- export.for.toxvaldb.manuscript, 13
- export.missing.dictionary.entries, 14
- export.missing.strains, 14
- export.missing.toxval_type, 15
- export.toxvaldb.subset, 15
- export.update.source.info, 16
- fill.chemical.by.source, 16
- fill.toxval.defaults, 17
- fill.toxval.defaults.global.by.source, 17
- filter, 39, 61
- fix.all.param.by.source, 18
- fix.associated.pod.critical_effect, 18
- fix.casrn, 19
- fix.critical_effect.icf.by.source, 20
- fix.dedup.hierarchy.by.source, 20
- fix.derived.toxval_type.by.source, 21
- fix.empty.by.source, 22
- fix.empty.record_source.by.source, 22
- fix.exposure.params, 23
- fix.generation.by.source, 23
- fix.human_eco.by.source, 24
- fix.non_ascii.v2, 24
- fix.priority_id.by.source, 25
- fix.qc_status.by.source, 26
- fix.replace.unicode, 26
- fix.risk_assessment_class.by.source, 27
- fix.single.param.by.source, 28
- fix.species.common_name, 28
- fix.species.duplicates, 29
- fix.species.v2, 29
- fix.strain.v2, 30
- fix.study_duration.params, 30
- fix.study_group, 31
- fix.study_type.by.source, 32
- fix.trim_spaces, 33
- fix.units.by.source, 33
- flush.console, 37, 42
- generate originals, 34
- GET, 39
- getDBConn, 35
- group_by, 61
- import.dictionary, 35
- import.source.info.by.source, 36
- is.cas, 5

keep, [39](#)

load.dsstox, [36](#)
log_message, [37](#)

mutate, [39](#), [61](#)

na_if, [61](#)

pivot_longer, [39](#)
printCurrentFunction, [37](#)
pull_jira_info, [38](#)

qa_toxval_url_validation, [39](#)

read.xlsx, [25](#)
read_excel, [39](#)
reexports, [19](#), [39](#), [61](#)
runInsert, [40](#)
runInsertTable, [41](#)
runQuery, [42](#)
runStatement, [43](#)
runUpdate, [44](#)

select, [61](#)
set.critical_effect_category, [45](#)
set.experimental_record.by.source, [45](#)
set.initial.qc_status, [46](#)
set.qc.category.by.source, [46](#)
set.study_type.by.study_group, [47](#)
set.supersource.export.names, [48](#)
set_extraction_doc_cldower_id, [48](#)
set_toxval_relationship_by_toxval_type, [49](#)

source_chemical.chemidplus, [49](#)
source_chemical.ecotox, [50](#)
source_chemical.extra, [51](#)
source_chemical.toxrefdb, [51](#)
source_hash_vectorized, [52](#)
species.qc, [53](#)
species.strain.mismatch, [53](#)
status_code, [39](#)
str_detect, [6](#)
str_pad, [6](#)
str_trim, [8](#), [25](#)
stri_escape_unicode, [25](#)
summarise, [61](#)

toxval.config, [54](#)
toxval.init.db, [55](#)
toxval.load.alaska_dec, [55](#)
toxval.load.all, [56](#)
toxval.load.atsdr.pfas.2021, [57](#)
toxval.load.atsdr_mrls, [57](#)
toxval.load.caloehta, [58](#)
toxval.load.cancer, [58](#)
toxval.load.chemidplus, [59](#)
toxval.load.copper, [60](#)
toxval.load.dedup, [60](#)
toxval.load.dod, [61](#)
toxval.load.doe.benchmarks, [62](#)
toxval.load.doe.pac, [62](#)
toxval.load.echa_iuclid, [63](#)
toxval.load.ecotox, [64](#)
toxval.load.efsa, [64](#)
toxval.load.epa_aegl, [65](#)
toxval.load.epa_hhtv, [65](#)
toxval.load.epa_ow_npdwr, [66](#)
toxval.load.epa_ow_nrwqc_hhc, [66](#)
toxval.load.generic, [67](#)
toxval.load.genetox.all, [68](#)
toxval.load.gestis.dnel, [68](#)
toxval.load.hawc, [69](#)
toxval.load.hawc_pfas_150, [69](#)
toxval.load.hawc_pfas_430, [70](#)
toxval.load.healthcanada, [70](#)
toxval.load.heat, [71](#)
toxval.load.hess, [72](#)
toxval.load.hpvis, [72](#)
toxval.load.initial, [73](#)
toxval.load.iris, [73](#)
toxval.load.mass_mmcl, [74](#)
toxval.load.niosh, [74](#)
toxval.load.ntp.pfas, [75](#)
toxval.load.opp, [75](#)
toxval.load.osha_air_limits, [76](#)
toxval.load.ow_dwsa, [76](#)
toxval.load.penn, [77](#)
toxval.load.penn_dep_mscs, [77](#)
toxval.load.pfas_150_sem_v2, [78](#)
toxval.load.postprocess, [78](#)
toxval.load.pprtv.cphea, [79](#)
toxval.load.rsl, [80](#)
toxval.load.skin.eye, [80](#)
toxval.load.source_chemical, [81](#)
toxval.load.species, [81](#)
toxval.load.test, [82](#)
toxval.load.toxrefdb2.1, [82](#)

toxval.load.usgs_hbsl, [83](#)
toxval.load.ut_hb, [83](#)
toxval.load.who_ipcs, [84](#)
toxval.load.who_jecfa_adi, [84](#)
toxval.load.who_jecfa_tox_studies, [85](#)
toxval.set.mw, [85](#)
toxval.summary.stats, [86](#)
toxval_type.species.mismatch, [87](#)
toxvaldb.view, [86](#)

webchem, [5](#)
write.xlsx, [25](#)
write_excel, [39](#)