toxvaldbBMDh

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Type Package

Title Calculates BMDh Values From Records in ToxValDB

Version 2.0.0

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Description This package extracts data from the ToxValDB database, filters it
for redundant records (this redundancy should be reduced in later versions),
and calculates study-level and chemical-level BMD.
To run the entire process, uses the functions export.for.bmdh(), filter.for.bmdh(),
bmd.per.study(), bmd.per.chemical() and bmdh.percentile.plot(). The function driver() runs all of the
methods sequentially. The last function provides the best percentile to use.
All of the input and output data lives in the data/ folder

License BSD3

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Imports dplyr,
magrittr,
readxl,
stringr,
tidyr,
writexl

Contents

`bmdh.aurisano.check.plot`

bmdh.aurisano.check.plot

Description

Plot the difference between the Aurisano and current BMDh values

Usage

```
bmdh.aurisano.check.plot(
  to.file = FALSE,
  toxval.db = "res_toxval_v95",
  sys.date = Sys.Date()
)
```

Arguments

to.file	If TRUE, send the plot to a file
toxval.db	Database version
sys.date	The date of the database export

Details

DETAILS

Value

None; writes plot to PDF

See Also

read.xlsx ggplot, aes, labs, geom_point, ggtheme, scale_continuous, ggsave dev

Examples

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

## End(Not run)
```

---

bmdh.cumdist.plot *bmdh.cumdist.plot*

Description

Plot the cumulative distribution of number of studies

Usage

```
bmdh.cumdist.plot(
  to.file = F,
  toxval.db = "res_toxval_v95",
  sys.date = Sys.Date()
)
```

Arguments

to.file	If TRUE, send the plot to a file
toxval.db	Database version
sys.date	The date of the database export

Details

DETAILS

Value

writes a plot to a file

See Also

read.xlsx ggplot, aes, labs, stat_ecdf, ggtheme, lims, ggsave ggarrange dev

Examples

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

## End(Not run)
```

---

bmdh.per.chemical *bmdh.per.chemical*

Description

Calculate BMDh values one per chemical

Usage

```
bmdh.per.chemical(
  toxval.db,
  run_name = Sys.Date(),
 regulatory.sources = c("source_atsdr_mrls", "source_epa_hhtv", "source_health_canada",
    "source_iris", "source_heast", "source_pprtv_cphea")
)
```

Arguments

toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)
regulatory.sources	This is the list of sources that will be used to select the #' optimal quantile to use for selecting the final chemical-level BMDh.

Details

Calculates one BMDh value per chemical. This is done by taking various percentiles of the distribution of the BMDh values and building a table with one column per percentile per chemical. The values are calibrated against regulatory values. The list of high-quality, regulator sources is given as one of the calling arguments.

Value

Write a file with the results: toxval_PODs_for_BMDh chemical level toxval.db sys.date.xlsx

See Also

`read.xlsx`, `createStyle`, `write.xlsx` `sd`, `quantile`

Examples

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

## End(Not run)
```

`bmdh.per.study` *bmdh.per.study*

Description

Calculate the BMDh values per study

Usage

```
bmdh.per.study(toxval.db, run_name = Sys.Date())
```

Arguments

`toxval.db`	Database name
`run_name`	The desired name for the output directory (Default: current date)

Details

Calculates one BMDh value per study using the Aurisano algorithm. Because EPA has not fully developed the mapping from critical effects in ToxValDB to standardized effects, teh values from Aurisano are used where records match. Aurisano used ToxValDB 9.1, whereas 9.5 is used here. There is also code here to do the other required mappings, and thos may need to be updated.For records in both the old and new databases, an on-the-fly plot is produced to show the corresponded between study-level BMDh values.

Value

Write a file with the results: toxval_PODs_for_BMDh toxval.db sys.date.xlsx

See Also

read.xlsx, createStyle, write.xlsx plot.default

Examples

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

## End(Not run)
```

---

bmdh.percentile.plot *bmdh.percentile.plot*

Description

Plot the BMDs vs the regulatory values for different percentiles and determine the best fit

Usage

```
bmdh.percentile.plot(
  to.file = FALSE,
  toxval.db,
  run_name = Sys.Date(),
  minstudies = 3,
  cutoff.logsd = 2
)
```

Arguments

to.file	If TRUE, send the plot to a file
toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)
minstudies	- only chemicals with this minimum number of studies will be used in the calculation
cutoff.logsd	Only chemicals with their log SD of BMDh values will be used in the calculation

Details

Helps determine the optimal percentile. The output file shows the fit statistics for different percentiles, and one should select the one with the lowest RMSE and highest R2.

Value

Write a file with the results: toxval_PODs_for_BMDh chemical level toxval.db sys.date.xlsx

See Also

read.xlsx, write.xlsx lm character(0) ggplot, aes, labs, geom_point, ggtheme, facet_grid, lims, geom_segment, ggsave dev

Examples

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

## End(Not run)
```

---

check_dcap_toxicological_effect_category_mappings
check_dcap_toxicological_effect_category_mappings

Description

Attempts to remap previously-mapped toxicological_effect_category values to DCAP entries

Usage

```
check_dcap_toxicological_effect_category_mappings(
  toxval.db,
  get_suggestions = TRUE,
  input_file = "",
  output_dir = ""
)
```

Arguments

toxval.db	The version of ToxVal to use
get_suggestions	Whether to provide mapping suggestions (Default: TRUE)
input_file	The file to pull missing toxicological_effect_category from.
output_dir	The folder used to write output to

Details

The output Excel files are as follows: - dcap_mappings_identified.xlsx: All toxicological_effect_categories that could be confidently remapped - dcap_mappings_still_missing.xlsx: Full data for entries missing categorizations - dcap_missing_categorization.xlsx: Just toxicological_effect, study_type values missing categorizations - dcap_mapping_suggestions.xlsx: Mapping suggestions based on close, but not exact, matches

Value

None; output is written to Excel files

`convert.fields.to.json` *convert.fields.to.json*

Description

Combine non-ID columns from audit table into JSON format for audit storage

Usage

```
convert.fields.to.json(in_dat)
```

Arguments

`in_dat`	data to translate to JSON format

Details

DETAILS

Value

Values in JSON format

See Also

`summarise`, `select`, `bind` `toJSON`, `fromJSON`

Examples

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

## End(Not run)
```

convert_get_conversion_factor *convert_get_conversion_factor*

Description

A helper function to convert input values to desired units.

Usage

```
convert_get_conversion_factor(conv_factor = 1)
```

Arguments

conv_factor	Conversion factor to use (such as Molecular weight, tissue Density, etc.)

Details

DETAILS

Value

List of conversion factors

Examples

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

## End(Not run)
```

convert_units *FUNCTION_TITLE*

Description

A helper function to convert input values to desired units.

Usage

```
convert_units(x, units, desired, conv_factor = NA)
```

Arguments

x	Numeric to be converted
units	Original units to be converted
desired	Desired units to convert the input value into
conv_factor	Conversion factor to use (such as Molecular weight, tissue Density, etc.)
overwrite_units	Boolean to overwrite the 'units' with desired units.

Details

DETAILS

Value

OUTPUT_DESCRIPTION

Examples

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

## End(Not run)
```

---

dcap.counts *dcap.counts*

Description

Calculate some stats for DCAP

Usage

```
dcap.counts(toxval.db, run_name = Sys.Date())
```

Arguments

toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)

Details

Gets some statistics for the DCAP project off of the current ToxValDB export

Value

Write a file with the filtered results:ToxValDB for BMDh filtered toxval.db sys.date.xlsx

See Also

read.xlsx, write.xlsx

Examples

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

## End(Not run)
```

`driver` *driver*

Description

Run all of the calculations to go from database export to calculation of final BMDh values

Usage

```
driver(
  toxval.db,
  run_name = Sys.Date(),
  run.export = TRUE,
  include.pesticides = FALSE,
  include.drugs = FALSE,
  include.epa_dws = TRUE,
  include.food_add = FALSE,
  reset.study_group = FALSE
)
```

Arguments

`toxval.db`	Database name
`run_name`	The desired name for the output directory (Default: current date)
`run.export`	Whether to run the export.for.bmdh function (Default: TRUE)
`include.pesticides`	Flag to include pesticides in output or not
`include.drugs`	Flag to include drugs in output or not
`include.epa_dws`	Flag to include EPA DWS in output or not

include.food_add
: Flag to include food additives in output or not

reset.study_group
: Flag to reset study_group

Details

DETAILS

Value

None

Examples

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

## End(Not run)
```

`export.for.bmdh` *export.for.bmdh*

Description

Export records required for calculating BMDh values.

Usage

```
export.for.bmdh(
  toxval.db,
  include.pesticides = FALSE,
  include.drugs = FALSE,
  include.epa_dws = TRUE,
  include.food_add = FALSE,
  reset.study_group = FALSE,
  run_name = Sys.Date()
)
```

Arguments

toxval.db
: Database version

include.pesticides
: Flag to include pesticides in output or not

include.drugs
: Flag to include drugs in output or not

include.epa_dws
: Flag to include EPA DWS in output or not

include.food_add
: Flag to include food additives in output or not

reset.study_group
: Flag to reset study_group

run_name
: The desired name for the output directory (Default: current date)

Details

Exports all of the data required for the BMDh calculations. The main query may need to be modified to extract more columns if needed for the final application. Certain sources have been excluded because they have a high percentage of read-across values. Species are filtered to only include Human, Dog, Mouse, Rat and Rabbit. If more species are to be included, then allometric scaling factors for those need to added to the function bmd.per.study().

Value

Write a file with the results: ToxValDB for BMDh toxval.db Sys.Date().xlsx

See Also

createStyle, write.xlsx

Examples

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

## End(Not run)
```

---

export.for.toxicological_effect_mapping

export.for.toxicological_effect_mapping

Description

Export records required for managing the critical effect categories for the BMD calculations.

Usage

```
export.for.toxicological_effect_mapping(
  toxval.db = "res_toxval_v95",
  user = "rjudson",
  password
)
```

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.

Details

Exports all of the data required for performing the critical effect mapping for the BMDh calculations

Value

Write a file with the results: ToxValDB for BMDh toxval.db Sys.Date().xlsx

See Also

createStyle, write.xlsx

Examples

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

## End(Not run)
```

---

filter.pods *filter.pods*

Description

Filter values for BMDh according to specified POD rules

Usage

```
## S3 method for class 'pods'
filter(toxval.db, run_name = Sys.Date())
```

Arguments

toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)

Details

Filtering steps differ between authoritative and non-authoritative sources

Value

None; filtered results are recorded in Excel file

See Also

read.xlsx, createStyle, write.xlsx

Examples

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

## End(Not run)
```

---

filter.summary *filter.summary*

Description

Summarize the filtering steps

Usage

```
## S3 method for class 'summary'
filter(toxval.db, run_name = Sys.Date(), do.load = TRUE)
```

Arguments

toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)
do.load	Whether to load data from Excel, Default: TRUE

Details

Filters where multiple NOEL/NOEL etc. exist. For each study_group this will select the highest NO(A)EL below the lowest LO(A)EL and the lowest LO(A)EL. In all cases, all BMDx values are included

Value

Write a file with the filtered results:ToxValDB for BMDh LEL NEL multiNOEL filtered toxval.db sys.date.xlsx

See Also

read.xlsx, createStyle, write.xlsx

Examples

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

## End(Not run)
```

`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.study_group` *Set the study_group field*

Description

Set the study_group field

Usage

```
fix.study_group(df)
```

Arguments

`df`	Input dataframe to set study_group

Value

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

`get.conceptual_model.by.toxicological_effect_category` *get.conceptual_model.by.toxicological_effect_category*

Description

Get the conceptual model based on toxicological_effect_category

Usage

```
get.conceptual_model.by.toxicological_effect_category(df)
```

Arguments

`df`	Input dataframe of study_type and toxicological_effect data.

Details

DETAILS

Value

DataFrame map of models by toxicological_effect and study_type

See Also

`select`, `distinct`, `mutate`, `context`, `case_when`, `mutate-joins`, `rename`, `across`, `reexports`, `group_by`, `na_if` `separate_rows`, `replace_na` `str_trim` `read_delim`, `cols`

Examples

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

## End(Not run)
```

---

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)
```

---

get_chemcial_index *get_chemical_index*

Description

Generate a chemical index based on ToxVal DTXSID list and QSAR Ready Smiles.

Usage

```
get_chemcial_index(input_toxval_file, input_qsar_file)
```

Arguments

`input_toxval_file`
: Filepath to input ToxVal file with DTXSID values.

`input_qsar_file`
: Filepath to input QSAR Ready Smiles file with DTXSID values.

Details

DETAILS

Value

Combined chemical index dataframe. A CSV file is also written to the input subfolder.

See Also

`read_delim`, `cols`, `write_delim` `select`, `mutate-joins`, `distinct`, `c("rowwise", "rowwise")`, `mutate`, `group_by` `map` `digest`

Examples

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

## End(Not run)
```

`init.current.run.directory` *init.current.run.directory*

Description

Initialize output directory for current driver run

Usage

```
init.current.run.directory(run_name = Sys.Date())
```

Arguments

`run_name`	The desired name for the output directory (Default: current date)

Details

DETAILS

Value

None; new directory is created

Examples

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

## End(Not run)
```

`pod.per.chemical` *pod.per.chemical*

Description

Explore different methods for calculating PODs

Usage

```
pod.per.chemical(toxval.db = "res_toxval_v95", sys.date = Sys.Date())
```

Arguments

`toxval.db`	The version of ToxValDB to use
`sys.date`	Date of the most recent data export #' Make the rule #' filter LOELs when NOELs are present for the same study #' filter out redundant values for the same study group #' Perform the allometric scaling
`t2`	PARAM_DESCRIPTION
`scale.mat`	PARAM_DESCRIPTION

Details

Explore different methods for calculating PODs This uses the same input as the function bmdh.perstudy / bmdh.per.chemical

Value

Writes output to file

Examples

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

## End(Not run)
```

pod.per.chemical.eco *pod.per.chemical.eco*

Description

Calculate the eco PODs

Usage

```
pod.per.chemical.eco(toxval.db = "res_toxval_v95", sys.date = Sys.Date())
```

Arguments

toxval.db	The version fo the ToxValDB to use
sys.date	The date of the database export

Details

DETAILS

Value

Writes output to file

See Also

read.xlsx, write.xlsx quantile, sd

Examples

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

## End(Not run)
```

pod.rule.maker *pod.rule.maker*

Description

Function to create/choose rule based on POD inputs

Usage

```
pod.rule.maker(
  toxval,
  hra.sources,
  rule.name = "Rule 3",
  rule.stype = "chronic",
  rule.ttype = "LO(A)EL, NO(A)EL, BMD",
  stype.list = c("chronic"),
  ttype.list = c(loel.types, noel.types, bmdl.types)
)
```

Arguments

toxval	Input dataframe of ToxVal data.
hra.sources	Human Risk Assessment source list
rule.name	PARAM_DESCRIPTION, Default: 'Rule 3'
rule.stype	PARAM_DESCRIPTION, Default: 'chronic'
rule.ttype	PARAM_DESCRIPTION, Default: 'LO(A)EL, NO(A)EL, BMD'
stype.list	PARAM_DESCRIPTION, Default: c("chronic")
ttype.list	PARAM_DESCRIPTION, Default: c(loel.types, noel.types, bmdl.types)

Details

DETAILS

Value

Modified version of input toxval dataframe.

See Also

quantile, sd

Examples

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

## End(Not run)
```

`printCurrentFunction` *printCurrentFunction*

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)
```

property.counter *property.counter*

Description

Count proerties of records

Usage

```
property.counter(toxval.db = "res_toxval_v95", sys.date = Sys.Date())
```

Arguments

toxval.db	Database version
sys.date	The date of the database export
user	The username for the MySQL database. The database instance is #' hard-coded in the function setDBConn().
password	The user's MySQL database password.

Details

DETAILS

Value

Write a file with the results: ToxValDB for BMDh toxval.db Sys.Date().xlsx

See Also

read.xlsx, write.xlsx, createStyle

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)
```

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)
```

`split.species.list` *Split species list*

Description

Split species lists into multiple rows

Usage

```
## S3 method for class 'species.list'
split(df)
```

Arguments

`df`	Input dataframe with species lists to split

Details

DETAILS

Value

Modified input df with split species lists into multiple rows

See Also

`mutate`, `case_when`, `filter`, `bind_rows`, `group_by`, `summarise` `separate_rows` `str_trim`, `case`

Examples

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

## End(Not run)
```

`studies.per.chemical` *studies.per.chemical*

Description

Calculate some stats for DCAP

Usage

```
studies.per.chemical(toxval.db, run_name = Sys.Date())
```

Arguments

`toxval.db`	Database name
`run_name`	The desired name for the output directory (Default: current date)

Details

Gets the number of studies per chemical from the current ToxValDB export

Value

Write a file with the filtered results:ToxValDB for BMDh filtered toxval.db sys.date.xlsx

See Also

`read_xlsx`, `write_xlsx`

Examples

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

## End(Not run)
```

study_group.multichem *study_group.multichem*

Description

Find study groups that span multiple chemicals

Usage

```
study_group.multichem(toxval.db, run_name = Sys.Date())
```

Arguments

toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)

Details

DETAILS

Value

Write a file with the filtered results:ToxValDB for BMDh LEL NEL multiNOEL filtered toxval.db sys.date.xlsx

See Also

read.xlsx, createStyle, write.xlsx

Examples

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

## End(Not run)
```

`toxicological_effect_source` *toxicological_effect_source*

Description

Find the source for odd critical effect chunks.

Usage

```
toxicological_effect_source(toxval.db = "res_toxval_v95", user, password)
```

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.

Details

DETAILS

Value

Writes output to file

See Also

`read.xlsx`, `write.xlsx`

Examples

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

## End(Not run)
```

toxval.redundancies *toxval.redundancies*

Description

Detect potential redundancies in ToxValDB.

Usage

```
toxval.redundancies(toxval.db = "res_toxval_v95", user, password)
```

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.

Details

DETAILS

Value

Write a file with the results

See Also

createStyle, write.xlsx

Examples

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

## End(Not run)
```

`toxval.source.import.dedup` *toxval.source.import.dedup*

Description

Perform deduping on data before it is sent to toxval_source

Usage

```
toxval.source.import.dedup(
  res,
  dedup_fields = NULL,
  hashing_cols = NULL,
  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)
```

toxvaldb.statplots *toxvaldb.statplots*

Description

Plot statistics for ToxValDB for DCAP sources

Usage

```
toxvaldb.statplots(to.file = FALSE, toxval.db, run_name = Sys.Date())
```

Arguments

to.file	Whether to write plots to file or simply view them, Default: F
toxval.db	Database name
run_name	The desired name for the output directory (Default: current date)
dir	The directory where the lists are stored

Details

DETAILS

Value

None; plots are generated

See Also

read.xlsx ggplot, aes, labs, geom_boxplot, scale_continuous, scale_manual, coord_flip, ggtheme, theme, element, geom_jitter, geom_freqpoly, facet_wrap, lims, ggsave fct_rev reorder.default arrangeGrob dev

Examples

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

## End(Not run)
```

`write_dcap_summary` *write_dcap_summary*

Description

Output summary reports containing chemical and key field information

Usage

```
write_dcap_summary(toxval.db, sys.date = Sys.Date())
```

Arguments

`toxval.db`	The version of ToxVal to use
`sys.date`	The date of the export to use, Default: Sys.Date()

Details

DETAILS

Value

None; writes summary reports to file

See Also

[read_xlsx][readxl::read_xlsx] [mutate][dplyr::mutate], [filter][dplyr::filter], [select][dplyr::select], [distinct][dplyr::distinct], [left_join][dplyr::left_join], [pull][dplyr::pull], [ensym][dplyr::ensym] [replace_na][tidyr::replace_na] [tibble][tibble::tibble] [write.xlsx][openxlsx::write.xlsx]

Examples

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

## End(Not run)
```

`%>%` *Pipe operator*

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)‘.

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